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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                                                        July 21, 2000, 01:57:46; Search time 2513.97 Seconds (without alignments) 705.652 Million cell updates/sec
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                            - nucleic search, using sw model
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161345 Homo sapi
S659822 Homo sapi

Description

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AR037506 Sequence
141160 Sequence
1536844 Homo sapien
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LB1167 Rattus norv
S79760 Ink4 [rats,
AF044336 Mus muscu
AF044336 Mus muscu
AF04437697 Sequence
AR001317 Sequence
AR037497 Sequence
AR062777 Sequence
                                141150 Sequence 4
U12819 Human p16-I
U17075 Human p14-C
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Okamoto, A., Demetrick, D.J., Spillare, E.A., Hagiwara, K.,
Hussain, S.P., Bennett, W.P., Forrester, K., Gerwin, B., Serrano, M.
Beach, D.H. and Harris, C.C.
Mutations and altered expression of p16INK4 in human cancer
Proc. Natl. Acad. Sci. U.S.A. 91 (23), 11045-11049 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (01-SEP-1994) Manuel Serrano, Cold Spring Harbor
Laboratory, 1 Bungtown Road, Cold Spring Harbor, NY 11724, USA
On Oct 18, 1994 this sequence version replaced gi:535942.
Location/Qualifiers
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A new requiatory motif in cell-cycle control causing specific inhibition of cyclin D/CDK4
Nature 366 (6456), 704-707 (1993)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (02-JAN-1994) Manuel Serrano, Cold Spring
Laboratory, 1 Bungtown Road, Cold Spring Harbor, NY
4 (bases 1 to 987)
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AR062786
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TITLE
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HUMINK4X
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AGAGGCTCTGAGAAACCTCGGGAAACTTAGATCATCAGTCACCGAAGGTCCTACAGGGCC 540
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                                                                                            TTAAAAATGTCCTGCCTTTTAACGTAGATATAAGCCTTCCCCCACTACCGTAAATGTCCA
                                                          TTTATATATCATTTTTTATATATTCTTATAAAATGTAAAAAGAAAAAACACCGCTTCTGCC
                                                                                                                     TTTTCACTGTGTGTGGAGTTTTCTGGAGTGAGCACTCACGCCCTAAGCGCACATTCATGTG
                                                                                                                              GAACTAGGGAAGCTCAGGGGGGTTACTGGCTTCTCTTGAGTCACACTGCTAGCAAATGGC
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Probes for MTS1 gene and polynucleotides encoding spaceti US 5801236-A 36 01-SEP-1998;
Location/Qualifiers
1. .947
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Pred. No. 7.3e-151;
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Pred. No. 7.3e-151;
0; Mismatches 2;
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MTSIE1.beta. gene
Patent: US 5739027-A 36 14-APR-1998;
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41 ATGGATCCGGCGGGGGGGAGAGCATGGACTTCGGCTGACTGGCTGG	DD	401 CTGGGCCATCGCGATGTCGCACGTACCTGCGCGGGGGCGCGGGGGCACCAGAGGCACT [Db 481 AGAGGCTCTGAGAAACCTCGGGAAACTTAGATCATCAGTCACGGAGGTCCTACAGGGCC 540 Qy 581 ACAACTGCCCGCCACAACCCACCCCGCTTTCGTATTTAGAAAATAGAGCTT 640	Db 661 TITATATCATTTTTTATATATATATATATATATATATATA	RESULT 5 141180 LOCUS LOCUS DEFINITION Sequence 36 from patent US 5624819. ACCESSION 141180.1 GI:2081770 KEYWORDS SOURCE Unknown.
	OY 521 AGAGGCTCTGAGAAACTCGGGAAACTTAGATCATCAGTCCGAAGGTCCTACAGGGCC 580		OY 821 GGCATTTCTTGCGAGCCTCGCAGAGCTGTCGACTTCATGACAAGCATTTGT 880	AR062806 947 bp DNA PAT Sequence 36 from patent US 5843756. AR062806 AR062806.1 GI:5990497 UNROWN. 1 UNKNOWN. 1 UNKNOWN. 1 Unclassified. 1 (bases 1 to 947) Stone, S., Janay, P. and Kamb, A. Mouse MTSI gene Patent: US 5843756-A 36 01-DEC-1998; Patent: US 5843756-A 36 01-DEC-1998;	Aorganism="unknown" BASE COUNT 207 a 271 c 274 g 195 t ORIGIN Query Match Best Local Similarity 99.8%; Score 943.8; DB 5; Length 947; Bast Local Similarity 99.8%; Pred. No. 7.3e-151; Matches 945; Conservative, 0; Mismatches 2; Indels 0; Gaps 0;

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/protein_id="Aaa82236.1"
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IVIMLIRSORLGOQPLRRPEHDDGNPSGGAAAAPRRGAQLRRPRHSHPTRARRCPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="pl6INK4/MTS1"
/note="also called exon 0.18, substituted by alternative
splicing to pl6INK4 exon 1"
                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (10-MAY-1995) Christian-Jacques Larsen, Institut de
Genetique moleculaire, U-301 Inserm, 27, rue juliette Dodu, Paris
                                                                                                                                                                                                                          Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dasse; To 1017)

Duro, D., Bernard, O., Della Valle, V., Berger, R. and Larsen, C.J. A new type of pl6INK4/MTSI gene transcript expressed in B-cell malignancies
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/note="a frameshift between exon 1 (0.18) and exon
changed the ORF of p161NK4 gene."
                     GAACTAGGGAAGCTCAGGGGGGTTACTGGCTTCTCTTGAGTCACACTGCTAGCAAATGGC
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Human p16INK4/MTS1 mRNA, complete cds.
U26727
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/tissue_type="hematopoletic"
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1. 1017
/organism="Homo sapiens"
/db_xref="taxon:9606"
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/chromosome="9"
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Larsen, C.-J.
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                                             Kamb, A.
Unclassified.

Unclassified.

I (bases I to 947)
S Skolnick,M.H., Cannon-Albright,L.A. and Kam Germline mutations in the MTS gene Germline mutations in the MTS gene
AL Patent: US 5624819-A 36 29-APR-1997;
Location/Qualifiers

I. 947

I. 947
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Best Local Similarity 99.8
Matches 945; Conservative
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                       GCCCAACTGCGCCGACCCCGCCACTCTCACCCGACCCGTGCACGACGCTGCCCGGGGGGG
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MTSIE1. beta. gene'
MTSIE1. US 5739027-A 13 14-APR-1998;
Patent: US 5739027-A 13 14-APR-1998;
Location/Qualifiers
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Stone, S., Jiang, P. and Kamb, A.
Mouse MrSI gene
Patent: US 5843756-A 13 01-DEC-
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Ramb,A.
Probes for MTS1 gene and polynucleotides
Patent: US 5801236-A 13 01-SEP-1998;
Location/Qualifiers
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100.0%; Pred. No. 1.2e-126;
iive 0; Mismatches 0;
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Skolnick,M.H., Cannon-Albright,L.A. and
Germline mutations in the MTS gene
Patent: US 5624819-A 13 29-APR-1997;
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327 c 343 g
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Sequence 13 from patent
141159 1 GI:2081749
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                TAAAAATGTAAAAAAGAAAAAACACCGCTTCTGCCTTTTCACTGTGTTGGAGTTTTCTGGA
                                                              TGGCTTCTTGAGTCACACTGCTAGCAAATGGCAGAACCAAAGCTCAAATAAAAATAAA
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Pred. No. 1.9e-110;
); Mismatches 6;
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Gyurls,J. Lamphore,L. and Beach,D.
Inhibitors of cell-cycle progression,
Patent: US 5672508-A 1 30-SEP-1997;
Location/Qualifiers
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Sequence 1 from patent US 5672508.
167718 1 GI:2731253
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/db_xref="G1:1353570"
/tb_xref="G1:1353570"
/translat_ion="MGGGFCCGPSIQLRGQEWRCSPLVPKGGAAAAELGPGRGENMVR
RFLVTLRIRRACGPBRYRVFVVHTPRLTGEWAAPGAPAAAJVLMLLRSQRLGQQPLP
RRPGHDDGQRPSGGAAAAPRRGAQLRRPRHSHLTRARRCPGGLPGHAGGAAPGRGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (19-OCT-1995) Alban J. Linnenbach, The Wistar Institute,
3601 Spruce Street, Philadelphia, PA 19104, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukaryota; Metazoa; Catarrhini; Hominidae; Homo.

1 (bases 1 to 905)
Linnenbach,A.J.

mRNA isoform with alternate first exon-encoded sequences at the cyclin-dependent kinase inhibitor 2 (pl6IRK4/MYS1) locus and mapping analysis of the region by using long-PCR
                                                                                                                                                                                                                                                                                                    A PRI 05-JUN-1996 protein (CDKN2A) mRNA, complete cds.
            1120 AGAGGCAGTAACCATGCCCGCATAGATGCCGCGGAAGGTCCCTCAGACATCCCCGGATGA 1179
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AGAGGCAGTAACCATGCCCGCATAGATGCCGCGGAAGGTCCCTCAGACATCCCCGATTGA
                                                 512 AAGAACCAGAGAGGCTCTGAGAAACCTCGGGAAACTTAGATCATCAGTCACCGAAGGTCC
                                                                                                      572 TACAGGGCCACAACTGCCCCCCCCCACCCCCCCCTTTCGTAGTTTTCATTAGAAA
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="s205"
/clone_lib="FM454 melanocyte cDNA library of
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/cell_type="melanocyte"
38. .559
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/note="variant signal"
299 9
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Human hypothetical 18.1 kDa
U38945
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/map="9p21"
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38. .559
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 Length 905,
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Nature 368 (6473), 753-756 (1994)
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Score 551.2; DB 10;
Pred. No. 2.7e-84;
0; Mismatches 3;
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/db_xref="taxon:9606"
/cell_type="melanoma"
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Direct Submission

Submitted (15-SEP-1999) Department Of Chemistry And Biochemistry,
The University of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
On Sep 15, 1999 this sequence version replaced gi:5801678.

Location/Qualifiers
1. 34669
/Organism="Homo sapiens"
/db_aref="taxon:9606"
/chromosome="9"
                                                                                                                                           Direct Submission
Submitted (30-OCT-1996) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
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                                                                            p16/CDK-INK4 gene
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/clone="c66"
/note="Left Neighbor sequenced in this c
Neighbor sequenced in this center: c86.
a 7299 c 7336 g 9592 t
                                       2 (bases 1 to 34669)
Burian, D.M., Mitchell, N. and Roe, B.A.
Homo sapiens Cosmid Clone c66 encoding the (Unpublished 1 to 34669)
          Olopade, F. I. and Rowley, J.D.
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4 (bases 1 to 34669)
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                       /note="cyclin-dependent kinase 4 inhibitor"
|oln(569821:1:<192. .498,22. .35)
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Pred. No. 9e-74;
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47.1%; Score 467.8; DB 5; Length 471;
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                                                             AR001314 471 bp DNA
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Cell-cycle regulatory protein p16 cDNA.
Cell-cycle regulatory protein p16; cyclin-dependent kinase inhibitor;
CCR: gene therapy; transgenic animal; cancer; cell proliferation;
SS; ds.
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Tumour suppressor p16 coding sequence.

Tumour suppressor; p16; inhibitor; cyclin-dependent kinase 4; CDK4;

cancer cell; lung cancer; badder cancer; melanoma; restenosis; therapy;
anti-angiogenic activity; hyperproliferative disorder; ss.
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                                                                  CGCGGAAGGTCCCTCAGACATCCCCGATTGAAAGAACCAGAGAGGCTCTGAGAAACCTCG
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                       CGCGGAGCCCAACTGCGCCGACCCCGCCACTCTCACCCGACCCGTGCACGACGCTGCCCG
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Pred. No. 1e-211;
0; Mismatches 3;
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Sequence 987
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P-PSDB; W10627
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Human multiple tumour suppressor gene 1.
Human; multiple; tumour; suppressor; MTS1; cancer; diagnosis;
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An individual can be diagnosed as having a predisposition to cancer by detecting an alteration in the wild type multiple tumour suppressor (MTS) gene, using gene probes which hybridise to the MTS1 cDNA 700747. The above assay can also be used in the diagnosis and prognosis of melanoma, lymphoma, leukaemia and pancreas, breast and sequence 947 BP; 207 A; 271 C; 273 G; 196 T;
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                                          CAGCCTCCGGAAGCTGTCGACTTCATGACAATTTTGTGAACTAGGGAAGCTCAGGGG
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AACGTAGATATAAGCCTTCCCCCACTACCGTAAATGTCCATTTATATCATTTTTTATATA
                                                                      TTCTTRTAAAAATGTAAAAAAAAAAAAAACACCGCTTCTGCCTTTTCACTGTGTTGGAGTTT
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Multiple tumour suppressor: MTS1; cancer; diagnosis; assay;
predisposition; melanoma; leukaemia; lymphoma; prognosis;
pancreas; breast; thyroid; ds.
Homo saplens.
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Pred. No. 1.8e-203;
0; Mismatches 1;
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17-MAR-1995; U03537.
18-MAR-1994; US-214582.
18-MAR-1994; US-215687.
18-MAR-1994; US-215686.
14-APR-1994; US-227369.
01-JUN-1994; US-251938.
(MYRI-) MYRIAD GENETICS INC.
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99.9%;
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T00747;
08-MAY-1996 (first entry)
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Best Local Similarity 99.9
Matches 946; Conservative
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US-215086.
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US-487033.
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14-APR-1994; US-227369.
01-JUN-1994; US-251938.
17-MAR-1995; WO-U03316.
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18-MAR-1994;
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The present sequence the human multiple tumour suppressor gene (MTS1), useful in cancer diagnosis.

Sequence 947 BP; 207 A; 271 C; 274 G; 195 T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 947;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 943.8; DB 1;
Pred. No. 4.1e-203;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                         Skolnick MH
                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                     Cannon-Albright LA, Kamb A,
WPI; 97-258217/23.
P-PSDB; W19251.
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99.8%;
                                                                                                                                                                                                                                                                  (MYRI-) MYRIAD GENETICS INC (UTAH) UNIV UTAH RES FOUND
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Nes 945; Conservative
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18-MAR-1994; US-215086.
18-MAR-1994; US-227369.
14-APR-1994; US-227369.
01-JUN-1994; US-251938.
17-MAR-1995; WO-U03337.
07-JUN-1995; US-474177.
 saplens
                                                                                             29-APR-1997.
18-MAR-1994;
                                                                       US5624819-A
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mutation(s) and their treatment
Disclosure; Column 89-90; 72pp; English.

This DNA sequence encodes a variant of the human multiple tumour suppression protein, MTSI. The MTS gene locus is also referred to as the familial melanoma (MLM) gene locus, located on human chromosome 9p21.

Germ line mutations in MTS genes can be used in the diagnosis of predisposition to cancers, e.g. melanoma, leukaemia, astrocytoma, pliboblastoma, lymphoma, glioma, Hodgkin's lymphoma, CLL, and cancers of the pancreas, breast, thyroid, ovary, uterus, testis, kidney, stomach and rectum.
                                                                                                                                                                                                                                                                                                                                             Villo-1998 (first entry)
Human MTG1 cDNA variant.
MTS1; multiple tumour suppressor; diagnosis; cancer; germ-line mutation;
MTS1; multiple tumour suppressor; diagnosis; cancer; germ-line mutation;
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                                                                                                                                        195
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458
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US-251938.
WO-U03316.
                                                                  (MYRI-) MYRIAD GENETICS
                                                                     Kamb A;
WPI; 98-494842/42.
01-SEP-1998.
07-JUN-1995; 4
07-JUN-1995; 0
18-MAR-1994; 0
18-MAR-1994; 0
14-APR-1994; 0
                                                  01-JUN-1994;
17-MAR-1995;
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V5381;
V64 DEC-1998 (first entry)
Coding sequence 3 of the multiple tumour suppressor 1.
Multiple tumour suppressor 1; MTS-1; human; cancer; hybridisation; somatic mutation; gene therapy; ds.
              CCCGTGCACGACGCTGCCCGGGAGGGCTTCCTGGACACGCTGGTGGTGCTGCACCGGGCC
                                                                                                                                  GGGCGCGCGCTGCGCGATGCCTGGGGCCGTCTGCCCGTGGACCTGGCTGAGGAG
                                                                                                                                          ACAACTGCCCCGCCCACCACCCCCCCTTTCGTAGTTTTCATTTAGAAAATAGAGCTT
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                                                                         GAGCTGCTGCTGCTCCACGGCGCGGAGCCCAACTGCGCCCGACCCCGCCACTCTCACCCGA
                                                                                                                                                               ACAACTGCCCCCGCCACAACCCACCCCGCTTTCGTAGTTTTCATTTAGAAATAGAGCTT
                                                                                                                                                                                                                                                                                   TTAAAAATGTCCTGCCTTTTAACGTAGATATAAGCCTTCCCCCACTACCGTAAATGTCCA
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Claim 1: Fig 17, Tapp; English.

This is the nucleotide sequence of the invention. The MTS gene

Compared to the method of the invention. The MTS gene

Compared to the diagnosis and prognosis of human cancer, e.g. by

Compared sequences are those that are present in somatic mutations

Compared sequences are those that are present in somatic mutations

Compared sequences are those that are present in some therapy

Compared sequences are those that are present in patients. These

Compared sequences are those that are present in patients. These

Compared sequences are those that are present in patients. These

Compared sequences are those that are present in patients. These

Compared sequences are those that are present in patients. These

Compared sequences are the construct protein mimetics, also for therapeutic

Compared sequences are the sequence and the protein are the protein and the protein are the sequence of the sequenc
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Nucleic acids based on multiple tumour suppressor, MTS, sequences useful as hybridisation probes, primers and recombinant production of MTS in the diagnosis and treatment of cancers related to MTS
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07-JUN-1995; US-508733.
(MYRI-) HOSE GENETICS INC.
Jiang P, Kamb A, Stone S;
WPI; 99-044585/04.
Mouse multiple tumour suppressor gene segment - useful for primer
                                                     TTAAAAATGTCCTGCCTTTTAACGTAGATATAAGCCTTCCCCCACTACCGTAAATGTCCA
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CDNA encoding a human multiple tum
Human; multiple tumour suppressor
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Inhibitor of cyclin dependent kinase 4 (pl6INK4).
Cyclin: cyclin dependent kinase; CDK; oncogene; cancer; leukaemia; lymphoma; cell cycle; detection; identification; tumour virus; proliferating cell nuclear antigen; subunit; complex; ss; ds.
GAGCTGCTGCTCCACGCGCGGAGCCCAACTGCGCCGACCCCGCCACTCTCACCAAA
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The proposed transformation of a cell and developing inhibitors and detection of subunit components of cyclin complexes - used for diagnosing transformation of a cell and developing inhibitors and activators, partic for cancer treatment

Claim 15; Page 39-40; 45pp; English.

The cell cycle gene implicated most strongly in oncogenesis is the human cyclin Di. It is genetically linked to the bcl-1 oncogene, a locus activated by translocation to an immunoglobulin gene enhancer. In some B-cell lymphomas and leukaemias. D-type cyclin, cyclin of polypeptide) exist in a quaternary complex that many combinatorial variations of the components e.g. cyclin Di or D3 and combinatorial variations of the components e.g. cyclin Di or D3 and combinatorial variations of the components e.g. cyclin Di or D3 and complexes. In virally transformation by DNA tumour viruses such as SV40 is associated with selective subunit rearrangement of the cyclin D complexes. In virally transformed cells, CDK4 totally dissociates from cyclin, PCNA and p21 and becomes associated with a 16 kilodalton polypeptide (p16). This nucleotide sequence encodes a 16 kba protein, designated p161NK4 which binds to and inhibits CDK4. This polypeptide was discovered to show many similarities to p16.

Reagents, such as monoclonal antibodies, can be developed that recognise the interactions between the CDK's cyclins, PCNA and low molecular weight proposed to identify the state of transformation of a cell in the relation of a cell in the state of transformation of a cell in the ce
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No. 1e-201;
smatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             266 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94.3%; Score 937.6;
99.6%; Pred. No. 1e-2
iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             270 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the state of transformation of a cell. Sequence 948 BP: 215 A: 270 C;
                         18-CCT-1993; U09945.
16-CCT-1992; US-963308.
17-DEC-1992; US-991997.
(CCLD-) COLD SPRING HARBOR LAB.
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Best Local Similarity 99.6
Matches 940; Conservative
                                                                                       Beach DH, Xiong Y;
WPI; 94-151320/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                      CCTGCCTTTTAACGTAGATATAAGCCTTCCCCCACTACCGTAAATGTCCATTTATATCAT
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Multiple tumour suppressor 1 exon 1 beta (MTSIElbeta) gene ORF.
Multiple tumour suppressor: MTSIElbeta: cancer: diagnosis; assay;
predisposition; melanoma; leukaemia; lymphoma; prognosis;
pancreas; breast; thyroid; open reading frame; ORF; exon 1; ds.
                                                                                 CCGCCACCACCCACCCCGCTTTCGTAGTTTTAGAAAATAGAGCTTTTAAAAATGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Pred. No. 4.7e-171;
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338. .655
/*tag= a
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(UTAH ) UNIV UTAH RES FOUND.
Cannon-Albright LA, Kamb A,
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18-MAR-1995; U03537.
18-MAR-1994; US-214582.
18-MAR-1994; US-215087.
18-MAR-1994; US-215086.
14-APR-1994; US-227369.
01-JUN-1994; US-221389.
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P-PSDB; R81700.
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Best Local Similarity
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03-MAY-1996 (first entry)
Human MTS polypeptide, MTSIEL-beta encoding cDNA.
Multiple tumour suppressor; E1-alpha; diagnosis; cancer; leukaemia; astrocytoma; glioblastoma; Hodgkin's lymphoma; melanoma; glioma; gene therapy; chronic; ds.
Homo sapiens.
                                                                                                                                                                                                                                                                                CCAGGTCATGATGATGGCCAGCGCCCGAGTGGCGGAGCTGCTGCTGCTCCACGGCGCGCGAA
                                                                              CGCTTTCGTAGTTTTCATTTAGAAAATAGAGCTTTTAAAAAATGTCCTGCCTTTTAACGTA
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Claim 4; Page 100-101; 156pp; English.

Craim 501peptides have been isolated asequenced. This sequence encodes polypeptides have been isolated (R80947). MTS polypeptide-encoding converse of the MTS polypeptide with the diagnosis or prognosis of human cancer. Germ-line mutations of MTS cohas can be used for human cancer. Germ-line mutations of MTS cohas can be used for diagnosing predisposition to melanoma, leukaemia, astrocytoma, glioma, glioma, Hodgkin's lymphoma, CLL and cancers of the pancreas, thyroid, ovary, uterus, testis, kidney, stomach and rectum. The wild-type gene is useful for gene therapy and MTS polypeptides may also be used for protein replacement therapy. Also creming for potential cancer therape may also be used for protein replacement therapy. Also screening for potential cancer therape may 327 C; 343 G; 229 T;
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therapy of
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Wild-type multiple tumour
28-SEP-1995; U03316, 17-MAR-1995; U03316, 18-MAR-1994; US-214581, 18-MAR-1994; US-215086, 18-MAR-1994; US-215088, 18-MAR-1994; US-215087, US-251938, US-25
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CGCTTTCGTAGTTTTCATTTAGAAATAGAGCTTTTAAAAATGTCCTGCCTTTAACGTA 666
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                                                                                                         GATATAAGCCTTCCCCCACTACCGTAAATGTCCATTTATATCATTTTTTTATATATTTTTA 870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               V11249 standard; cDNA; 1131 BP.
V11249;
V11249;
Human MTSIE1-beta cDNA.
MTSIE1-beta; multiple tumour suppressor; diagnosis; cancer;
MTSIE1-beta; multiple fumour suppressor; diagnosis; cancer;
Human MTSIE1-beta; multiple fumour suppressor; diagnosis; cancer;
Homo sapiens.
                               CTGGGGCCGTCTGCCCGTGGACCTGGCTGAGGAGCTGGGCCATCGCGATGTCGCACGGTA
                                                                                                                                                                                                           TTAGATCATCAGCACGAAGGTCCTACAGGGCCACAACTGCCCCCGCCACAACCCACACCC
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                                                                                                                                                                                 AGGTCCCTCAGACATCCCCGATTGAAAGAACCAGAGAGGCTCTGAGAAACCTCGGGAAAC
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                                                                               CCTGCGCGCGCGTGCGGGGGCACCAGAGGCAGTAACCATGCCCGCATAGATGCCGGGGA
     DNA specific for Multiple Tumour Suppressor 1E1-beta gene
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338. .655
/*tag- a
/product- MTSIE1-beta
/note- "multiple tumour suppressor"
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US-215086.
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US-227369.
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WPI; 98-250421/22.
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                          TAAAAATGTAAAAAGAAAAACACCGCTTCTGCCTTTTCACTGTGTGGAGTTTTCTGGA
                                                                                                    GTGAGCACTCACGCCCTAAGCGCACATTCATGTGGGCATTTCTTGCGAGCCTCGCAGCCT
                                                                                                                            TGGCTTCTCTTGAGTCACACTGCTAGCAAATGGCAGAACCAAAGCTCAAATAAAAATAAA
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Disclosure; Columns 73-74; 72pp; English.
The present sequence the human multiple tumour suppressor gene (MTS1) Elbeta, useful in cancer diagnosis.
Sequence 1131 Bp; 232 A; 327 C; 343 G; 229 T;
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Human; multiple; tumour; suppressor; MTS1; cancer; diagnosis;
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338. .655
/*tag= a
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18-MAR-1994; US-214582.
18-MAR-1994; US-215086.
18-MAR-1994; US-215086.
14-APR-1994; US-227369.
01-JUN-1994; US-227369.
17-MAR-1995; WG-251938.
17-MAR-1995; WG-251938.
(MYRI-) MXRIAD GENETICS INC.
(UTAH) UNIV UTAH RES FOUND.
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P-PSDB; W19254
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Query Match
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     mutation(s) and their treatment.
Claim 1; Fig 12; 72pp; English.
This coNA sequence encodes a human multiple tumour suppression protein,
MTSIE1-beta. The MTS gene locus; located on human chromosome 9p21. Germ line
matations in MTS genes can be used in the diagnosis of predisposition to
ancers, e.g. melanoma, Leuksemia, astrocytoma, gliboblastoma, lymphoma,
glioma, Hodokin's lympho, leuksemia, storocytoma, gliboblastoma, lymphoma,
thyroid, ovary, uterus, testis, kidney, stomach and rectum.
Sequence 1131 BP; 232 A; 327 C; 343 G; 229 T;
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                                                                                                                        Length 1131;
to MTS1E1-beta
                                                                                                                                          0; Indels
                                                                                                                       80.6%; Score 801; DB 1; Le
100.0%; Pred. No. 4.7e-171;
tive 0; Mismatches 0;
for the diagnosis of cancers related
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Best Local Simi
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Example 7: Column 73-76; 73pp; English.

This is the nucleotide sequence of the multiple tumour suppressor

(MTSIEIS) gene, used in the method of the invention. The MTS gene
(MTSIEIS) gene, used in the method of the invention. The MTS gene
(Standard nucleic hybridisation techniques, of patient samples.)

The mutated sequences are those that are present in somatic mutations

of the gene in cancers. The vectors can be used for gene therapy

strategies to replace function of mutated protein in patients. These

can also be used to construct protein minetics, also for therapeutic

strategies. In addition the expression constructs can also be used

for recombinant production of MTS. Recombinant MTS can be used to

screen for drugs to be used for cancer therapy, and the protein

careen for drugs to be used for cancer therapy, and the protein

screen for drugs to be used for cancer therapy, and the protein

screen for drugs to be used for cancer therapy, and cell.

Sequence 1131 BP; 232 A; 327 C; 343 G; 229 T;
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                                                     04-DEC-1998 (first entry)
Coding sequence 1 of the multiple tumour suppressor MTSIEIS.
Multiple tumour suppressor; MTSIEIS; human; cancer; hybridisation; somatic mutation; gene therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acids based on multiple tumour suppressor, MTS, sequences useful as hybridisation probes, primers and recombinant production of MTS in the diagnosis and treatment of cancers related to MTS
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100.0%; Pred. No. 4.7e-171;
iive 0; Mismatches 0;
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/*tag= a
/product= "human MTSIE1S"
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standard; cDNA; 1131
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18-MAR-1994; US-214086.

18-MAR-1994; US-215087.

14-APR-1994; US-227369.

01-JUN-1994; US-227369.

17-MAR-1995; WO-U03316.
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US-480810.
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             CCAGGTCATGATGATGGGCAGCGCCCGAGTGGCGGAGCTGCTGCTGCTCCACGGCGCGGA
                                                                                CTTCCTGGACACGCTGGTGGTGCTGCACCGGGCCGGGGCGCGGGCTGGACGTGCGGATGC
                                                                                                                              CTGGGGCCCGTCTGCCCGTGGACCTGAGGAGCTGGGCCATCGCGATGTCGCACGGTA
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The present sequence encodes a human multiple tumour suppressor IEI-beta (MTSIEI-beta) protein. Primers designed from the gene can be used to design primers to detect abnormalities i.e. polymorphisms which may predispose towards malignancies such as melanoma, leukaemia, astrocytoma, lymphoma, glioma, as well as tumours of e.g. the breast,
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                    AGGTCCCTCAGACATCCCCCGATTGAAAGAACCAGAGAGGCTCTGAGAAACCTCGGGAAAC
                                                                    CGCTTTCGTAGTTTTCATTTAGAAATAGAGCTTTTAAAAATGTCCTGCCTTTTAACGTA
                                                                             TAAAAATGTAAAAAAAAAAAACACCGCTTCTGCCTTTTCACTGTTGGAGTTTTCTGGA
                                                                                                                                                                          GTGAGCACTCACGCCCTAAGCGCACATTCATGTGGGCATTTCTTGCGAGCCTCGCAGCCT
                                                                                                                                                                                                                        GTGAGCACTCACGCCCTAAGCGCACATTCATGTGGGGCATTCTTGCGAGCCTCGCAGCCT
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Local Similarity 100.0%; Pred. No. 4.7e-171;
les 801; Conservative 0; Mismatches 0; Indels
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CDNA encoding a human multiple tumour suppressor lEl-beta p
Human; multiple tumour suppressor l gene; MTS1; cancer; ds.
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Sequence 1131 BP; 231 A; 327 C
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/*tag= a
/product= MTSlEl-beta
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28-JUL-1995; US-508735.
07-JUN-1995; US-487033.
(WKRL-) MYRIAD GENETICS INC.
Jiang P, Kamb A, Stone S;
WPI; 99-044585/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                   standard; cDNA; 1131
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16-MAR-1998 (first entry)

CDK inhibitory fusion protein coding sequence #1.

CDK inhibitory fusion protein coding sequence #1.

Fusion gene; CDK inhibitor; cyclin-dependant kinase; p27 gene; p16 chimaric polypeptide; human; binding motif; proliferation control; cell differentiation; cell-cycle inhibitor; proliferative disorder; Homo sapiens.
                                                                                                                                                                                                                                                                   /*tag= b
/note= "poly-His tag"
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4. .1179
/*tag= a
4. .24
ВР
                                                                                           T74051 standard; cDNA; 1420 T74051;
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786 930

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This sequence encodes a chimmeric polypeptide of the invention. It was derived from a fusion of the human p27 and p16 cDNA sequences. The chimmeric polypeptides of the invention have cyclin-dependent Kinase (CDK) binding motifs from at least two different proteins that bind to CDKS. The protein controls proliferation and/or differentiation of cDKS. The protein controls proliferation and/or differentiation of cells, particularly they inhibit cell-cycle progression. They can be used to treat a wide range of proliferative disorders, e.g. cancer, leukaemia, psoriasis, atherosclerosis, restenosis, chronic inflammation etc. They can also treat diseases associated with de-differentiation of control can also treat diseases associated with de-differentiation of control con
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/note= "(Gly4Ser)2 linker"
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                                                                                                                                                                          (MITO-) MITOTIX INC.
Beach D, Gyurls J, Lamphere L;
WPI; 97-393685/36.
P-PSDB; W23534.
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17-JAN-1997; U00569.
23-JAN-1996; US-589981.
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Search completed: July 21, 2000, 06:18:38 Job time: 13635 sec Appli Appli Appli Appli Appli Appli Appli Appli

Sequence Seq

Sequence 4, A Sequence 15, Sequence 15, Sequence 15, Sequence 15,

81-918A-34

Run on:

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Sequence 1, Application US/08627610

Patent No. 5919997

GENERAL INFORMATION:

APPLICANT: Beach, David H.

APPLICANT: Serrano, Manuel

APPLICANT: Serrano, Manuel

APPLICANT: Serrano, Manuel

TITLE OF INVENTION: Transgenic Animals Having Modified Cell-Cycle

TITLE OF INVENTION: Regulation

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COCKFIELD

STREET: 60 State Street

CITY: Boston

STREET: MA

COMPUTE: MA

COMPUTE: NA

SOCIUMEN: USA

IPPE: FLOPPY disk

COMPUTER: BAPPE COMPAIN:

SOFTWARE: ASCIDI(text)

COMPUTER: ASCIDI(text)

COMPUTER: ASCIDI(text)

COMPUTER: ASCIDI(text)

COMPUTER: ASCIDI(text)

COMPUTER: ASCIDI(text)

SOFTWARE: ASCIDI(text)

CLASSIFICATION NUMBER: 36,709

RESERRACE, MARTHOW P.

STELEPLOM NUMBER: 36,709

REFERENCE, DOKET NUMBER: 36,709

REF
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ALIGNMENTS
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Copyright (c) 1993 - 2000 Compugen Ltd.
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RESULT 2 US-08-306-511A-1

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                                                                                                                                                and
Sequence 1, Application US/08306511A
Patent No. 5962316
GENERAL INFORMATION:
APPLICANT: Beach, David H.
APPLICANT: Demetrick, Douglas J.
APPLICANT: Hannon, Manuel
APPLICANT: Hannon, Gregory J.
TITLE OF INVENTION: Cell-Cycle Regulatry Proteins,
ATTILE OF INVENTION: Related Thereto
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: CSI-001CP2
TELECAMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
ITELEPHONE: (617) 227-5941
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 994 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/306,511A
FILING DATE: 14-SEP-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                            ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 100. Matches 994; Conservative
                                                                                                                                                                                    NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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: LOCATION:
US-08-306-511A-1
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                                          ACGGTACCTGCGCGCGCGCGGGGGCCACCAGAGGCAGTAACCATGCCCGCATAGATGC
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Patent No. 5968821
GENERAL INFORMATION:
APPLICANT: Beach, David H.
APPLICANT: Demetrick, Douglas J.
APPLICANT: Serrano, Manuel
APPLICANT: Serrano, Manuel
APPLICANT: GIIVENTION: Cell-Cycle Regulatory Proteins, TITLE OF INVENTION: and Uses Related Thereto NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 961 AATAAAATTATTTTCATTCATTCACTCAAAAAA 994
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/08/893,274
FILING DATE: 15-JULY-1997
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSE: FOLEY, HOAG & ELIOT LLP
STRET: One Post Office Square
CIT: Boston
STATE: MA
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                           NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIV-071.09
RELECHONE: (617) 832-1000
TELEPHONE: (617) 832-1000
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 994 base pairs
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/306,511
FILING DATE: 14-SEPTEMBER-1994
PRIOR APPLICATION DATA:
APPLICATION NAMER: US 08/248,812
FILING DATE: 25-MX-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,371
FILING DATE: 14-APRIL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/154,915
FILING DATE: 18-NOVEMBER-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/991,997
FILING DATE: 17-DECEMBER-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/991,997
FILING DATE: 16-OCTOBER-1992
ATPORNEY AGENT INFORMATION:
NAME: Viscort Watthon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 994 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 100.
Matches 994; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: CDNA
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; LOCATION: 41..508
US-08-893-274-1
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              CAGCCTCCGGAAGCTGTCGACTTCATGACAAGCATTTTGTGAACTAGGGAAGCTCAGGGG
CGCGGAAGGTCCCTCAGACATCCCCGATTGAAAGAACCAGAGAGGCTCTGAGAAACCTCG
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APPLICANT: Beach, David H.
APPLICANT: Beach, David H.
APPLICANT: Bernano, Manuel
APPLICANT: Serrano, Manuel
APPLICANT: Hannon, Gregory J.
TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses
TITLE OF INVENTION: Related Thereto
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley, Hoag & Eliot
STREET: One Post Office Square
CITY: Boston
STREET: One Post Office Square
CITY: Boston
STREET: NAA
COUNTY: USA
IPP: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPead
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/581,918A
FILING DATE: 02-JAN-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US.08/497,214
FILING DATE: 30-UN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/346,147
FILING DATE: 29-NOV-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/08581918A Patent No. 6043030 GENERAL INFORMATION:
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US-08-581-918A-1
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FILING DATE: 14-SEP-1994

PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
FILING DATE: 25-MAY-1994

PRIOR APPLICATION DATA:
APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,371

FILING DATE: 14-APR-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/154,915

FILING DATE: 18-NOV-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/991,997

FILING DATE: 17-DEC-1992

ATTORNEY/AGENT INFORMATION:
NAME: VINCENT, MATCHAW P.
REGISTRATION NUMBER: 36,709

REFERENCE/DOCKET NUMBER: 36,709

REFERENCE/DOCKET NUMBER: 36,709

REFERENCE/TON INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATIO
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TYPE: nucleic acid
STRANDEDNESS: both
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FEATURE:
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US-08-581-918A-1
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GENERAL INFORMATION:
APPLICAMY:
TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses:
TITLE OF INVENTION: Related Thereto
NUMBER OF SEQUENCES: 10
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                         AATAAAATTATTTCATTCACTCACTCAAAAAA 994
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CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/346,147
FILING DATE: 29-NOV1994
PRIOR APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 14-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/248,812
FILING DATE: 25-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,371
FILING DATE: 14-APR-1994
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 994 base pairs
LENGTH: 994 base pairs
LENGTH: 994 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
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MOLECULE TYPE: CDNA
FEATURE:
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LOCATION:
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 Length 994
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                    0; Mismatches
 Score 994;
Pred. No. 4
100.0%;
                   Matches 994; Conservative
           Similarity
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APPLICANT: Skolnick, Mark H.
APPLICANT: Skolnick, Mark H.
APPLICANT: Cannon-Albright, Lisa A.
APPLICANT: Kamb, Alexander.
ITILE OF INVENTION: GERMLINE MUTATIONS IN THE MTS GENE
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS: MISSEE: Vanable, Baetjer, Howard & Civiletti, LLP STREET: 1201 New York Avenue, Suite 1000 CITY: Washington STATE: DC COTTWENT OF THE COTTWENT OF THE TRANSPORTED TO THE TRANSPORTED TO THE TRANSPORTED TO THE TRANSPORT CURRENT APPLICATION DATA:

SOFTWARE PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/474,177
FILING DATE: 07-JUN-1995
PRIOR APPLICATION NUMBER: US/08/474,177
PRIOR APPLICATION NUMBER: US/08/474,177
PRIOR APPLICATION NUMBER: US/08/251,938
FILING DATE: 17-MAR-1995
PRIOR APPLICATION NUMBER: US/08/251,988
FILING DATE: 18-MAR-1994
PRIOR APPLICATION NUMBER: US/08/215,087
FILING DATE: 18-MAR-1994
PRIOR APPLICATION NUMBER: US/08/215,086
FILING DATE: 14-APR-1994 "Splice site acceptor. FEATURE:
NAME/KEY: misc_feature
LOCATION: 458
OTHER INFORMATION: /note= "Splice site acceptor. PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-MAR-1994
ATTONEY AGENT: 1NFORMATION:
NAME: Inhen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REGISTRATION NUMBER: 24,884-109348-E
TELECOMMUNICATION:
TELEPHONE: 202-962-4810
TELEFAX: 202-962-4830 961 AATAAAATTATTTTCATTCACTCAAAAAA 994 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS Sequence 36, Application US/08474177 Patent No. 5624819 OTHER INFORMATION: /note-Floppy disk TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 947 base pairs NAME/KEY: misc_feature ORGANISM: Homo sapiens COMPUTER READABLE FORM: MEDIUM IYPE: Floppy TYPE: nucleic acid STRANDEDNESS: doub TOPOLOGY: linear MOLECULE TYPE: CDN GENERAL INFORMATION: S ORIGINAL SOURCE: USA ANTI-SENSE: NO HYPOTHETICAL: 20005 US-08-474-177-36 LOCATION: COUNTRY:

580 840 940 640 880 280 340 300 400 460 520 480 600 700 99 760 820 Gaps 101 GCCCGGGGTCGGGTAGAGGAGGTGCGGGCGCTGCTGGAGGCGGTGGCGCTGCCCAACGCA 160 GGGGCGCGCTGGACGTGCGCGATGCCTGGGGCCGTCTGCCCGTGGACGTGGACGTGAGGAG 360 AACCATGCCCGCATAGATGCCGCGGAAGGTCCCTCAGACATCCCCGGATTGAAAGAACCAG TTTTCACTGTGTTGGAGTTTTCTGGAGTGAGCACTCACGCCCTAAGCGCACATTCATGTG GAACTAGGGAAGCTCAGGGGGGTTACTGGCTTCTCTTGAGTCACACTGCTAGCAAATGGC CCGAATAGTTACGGTCGGAGGCCGATCCAGGTCATGATGATGGGCAGCGCCCGAGTGGCG CCCGTGCACGACGCTGCCCGGGAGGCTTCCTGGACACGCTGGTGGTGCTGCACCGGGCC 341 GGGGCGCGCTGGACGTGCGCGATGCCTGGGGCCGTCTGCCCGTGGACCTGAGGAG CTGGGCCATCGCGATGTCGCACGGTACCTGCGCGGGGGCTGCGGGGGGGCACCAGAGGCAGT 521 AGAGGCTCTGAGAAACCTCGGGAAACTTAGATCATCAGTCACCGAAGGTCCTACAGGGCC ACAACTGCCCCCCCCCCCCCCCCCCCCCCCTTTCGTATTAGAAATAGAGCTT TTAAAAATGTCCTGCCTTTTAACGTAGATATAAGCCTTCCCCCACTACCGTAAATGTCCA GGCATTTCTTGCGAGCCTCGCAGCCTCCGGAAGCTGTCGACTTCATGACAAGCATTTTGT ó Length 947; Indels ; Score 943.8; DB 1; Pred. No. 3e-213; 0; Mismatches Query Match
Best Local Similarity 99.8%;
Matches 945; Conservative JS-08-474-177-36 191 481 641 281 301 401 461 421 581 701 761 721 821 881 ò 원 셤 ŏ ద 셤 δ 원 셤 ŏ ò g 셤 ŏ 셤 q ò 셤 g ŏ ò ò ă ŏ

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APPLICANT: Kamb, Alexander
ITILE OF INVENTION: MTS1 GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 8
US-08-480-810-36
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                                                              STATE: DC COUNTRY: USA
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; LOCATION: 458
; OTHER INFORMATION: /note= "Splice site acceptor.
US-08-487-033-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Splice site acceptor
                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 94.9%; Score 943.8; DB 2; Best Local Similarity 99.8%; Pred. No. 3e-213; Matches 945; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALLCAREL, DAME: Jeffrey L.
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24884-109348-C
TELECOMMUNICATION INFORMATION:
TRIEBHONE: 202-962-4810
Sequence 36, Application US/08487033
Patent No. 573907
GENERAL INFORMATION:
APPLICANT: Ramb, Alexander
TITLE OF INVENTION: MTSIE1-Beta GENE
NUMBER OF SEQUENCES: 36
COMBESSPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard &
                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/03316
FILING DATE: 17 MAR-1995
PRIOR APPLICATION NUMBER: PCT/US95/03316
FILING DATE: 01-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,086
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,369
FILING DATE: 14-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,369
FILING DATE: 14-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-MAR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/487,033
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 947 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
LOCATION: 151
OTHER INFORMATION: /note='
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: 202-962-8300
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MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
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ORIGINAL SOURCE
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841 GAACTAGGGAAGCTCAGGGGGGTTACTGGCTTCTCTTGAGTCACACTGCTAGCAAATGGC 900
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                  GCCCGGGGTCGGGTAGAGGAGGTGCGGGCGCTGCTGGAGGCGGGGGGGCGCTGCCCAACGCA 120
                                                                                                                                            181 GAGCTGCTGCTCCACGGCGCGGAGCCCAACTGCGCCGACCCCGCACTCTCACCGA
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                                                     CCGAATAGTTACGGTCGGAGGCCGATCCAGGTCATGATGATGGGCAGCGCCCGAGTGGCG
                                                                                                                          221 GAGCIGCIGCICCACGGCGCGGAGCCCAACIGCGCCGACCCCGCCACICICACCCGA
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APPLICANT: Stone, Steven
APPLICANT: Jiang, Ping
APPLICANT: Jiang, Ping
APPLICANT: Rang, Alexander
TITLE OF INVENTION: MTS GENE AND THERAPEUTIC USE THEREOF
NUMBER OF SEQUENCES: 47
ADDRESSES:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP STREET: 1201 New York Avenue, Suite 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 36, Application US/08508735; Patent No. 5843756; GENERAL INFORMATION:
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Pred. No. 3e-213;
0; Mismatches 2; Indels 0
            CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP STREET: 1201 New York Avenue, Suite 1000
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: /note= "Splice site acceptor." US-08-480-810-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: /note= "Splice site acceptor."
                                                                                                                                     COMPUTER READBALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DoS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 18-MAR. 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,369
FILING DATE: 14-APR.1994
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-MAR.1994
ATTORNEY/AGENT INFORMATION:
NAME: Inhen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24884-109348
TELEPONMUNICATION INFORMATION:
TELEPAX: 202-962-4810
                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/03316
FILING DATE: 17-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,938
FILING DATE: 01-70N-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,086
APPLICATION NUMBER: US 08/215,086
                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/480,810 FILING DATE: 07-JUN-1995 CLASSIFICATION: 435
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Best Local Similarity 99.8%;
Matches 945; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 947 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature LOCATION: 151
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
LOCATION: 458
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                                                STREET: 1
CITY: Was
STATE: DC
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APPLICANT: Skolnick, Mark H.
APPLICANT: Cannon-Albright, Lisa A.
APPLICANT: Cannon-Albright, Lisa A.
APPLICANT: Ramb, Alexander.
TITLE OF INVENTION: GERMLINE MUTATIONS IN THE MTS GENE AND
TITLE OF INVENTION: GENE
TITLE OF INVENTION: GENE
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                              GGGGCGCGCGCTGGACGTGCCGGATGCCTGGGGGCCGTCTGCCCGTGGACCTGGCTGAGGAG 360
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                                                         461 AACCATGCCCGCATAGATGCCGCGGAAGGTCCCTCAGACATCCCCGGATTGAAAGAACCAG
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                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/848,251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 36, Application US/08848251 Patent No. 5989815 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
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US-08-848-251-36
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241 CCCGTGCACGACGCTGCCCGGGAGGGTTCCTGGACACGCTGGTGGTGCTGCTGCACCGGGCC 300
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                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94.9%; Score 943.8; DB 3;
99.8%; Pred. No. 3e-213;
tive 0; Mismatches 2;
                                                                                                                                                                                                   PRIOR APPLICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US to be assigned
FILING DATE: 07-JUN-1995
PRIOR APPLICATION NUMBER: PCT/US95/0316
FILING DATE: 17-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 28,957
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAM: 202-962-8300
INFORMATION FOR SEC ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 947 Dass pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: /note-
US-08-508-735-36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
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Matches 945; Conservative
                                                     COMPUTER READABLE FORM:
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OTHER INFORMATION:
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                USA
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ANTI-SENSE: N
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SUFIMARE. CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,047
FILING DATE: 07-JUN-1995
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 5994095
GENERAL INFORMATION:
APPLICANT: Kamb, Alexander
ITLE OF INVENTION: MTS GENE
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
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SOFTWARE: PatentT
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Pred. No. 3e-213;
0; Mismatches 2; Indels 0;
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CHER INFORMATION: /note- "Splice site acceptor.
US-08-848-251-36
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                                                                                                                                                                                                                                                                                                                                                                                          24884-109348-G
                                                            PRIOR DATE: 1/-MAR-1999
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,938
FILING DATE: 01-UIN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,086
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,369
FILING DATE: 14-APR-1994
PRIOR APPLICATION NUMBER: US 08/214,582
FILING DATE: 11-APR-1994
APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-MAR-1994
APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-WAR-1994
                FILING DATE: 07-JUN-1995
APPLICATION NUMBER: PCT/US95/03537
FILING DATE: 17-MAR-1995
UMBER: US 08/474,083
07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 2488
TELECOMMUNICATION INFORMATION:
TELEFAN: 202-962-4810
TELEFAN: 202-962-8300
INFORMATION FOR SEQ ID NO: 36: SEQUENCE CHARACTERISTICS:
LENGTH: 947 base pairs
TENTE: nucleic acid
STRANDEDNESS: double
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                     NAME: Ihnen, Jeffrey L. REGISTRATION NUMBER: 28,957
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OTHER INFORMATION: /note-
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99.8%;
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Best Local Similarity 99.8
Matches 945; Conservative
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ANTI-SENSE: N
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APPLICATION NUMBER: PCT/US95/03316
FILLING DATE: 17-MAR-1995
FILLING APPLICATION DATA:
APPLICATION NUMBER: US 08/251,938
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AACCATGCCCGCATAGATGCCGCGGAAGGTCCCTCAGACATCCCCGATTGAAAGAACCAG
                     TTAAAAATGTCCTGCCTTTTAACGTAGATATAAGCCTTCCCCCACTACCGTAAATGTCCA
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1201 New York Avenue, Suite 1000
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APPLICATION UNMBER: US/09/120,130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 36, Application US/09120130
Patent No. 6037462
GENERAL INFORMATION:
APPLICANT: Kamb, Alexander
TITLE OF INVENTION: MTS1 GENE
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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PRIOR APPLICATION DATA:
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STREET: 1201 New
CITY: Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 20005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Splice site acceptor.
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Pred. No. 3e-213;
0; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CONTION: 458
COTHER INFORMATION: /note- "Splice site US-08-486-047-36
                                                                                                                                       PRICE AND CALLS.
PRICE APPLICATION DATA:
APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERNCE/DOCKET NUMBER: 24884-10934
TELEPHONE: 202-962-4810
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-MRR-1994
APPLICATION DATA:
APPLICATION NUMBER: US 08/215,086
FILING DATE: 18-MRR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,369
FILING DATE: 14-APR-1994
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Best Local Similarity 99.8%;
Matches 945; Conservative (
                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 36 SEQUENCE FURNATION FOR SEQ ID NO: 36 SEQUENCE FURNATERISTICS: LENGTH: 947 base pairs TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: linear MOLECULE TYPE: CDNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                               ANTI-SENSE: NO ORIGINAL SOURCE:
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                                                                                                                                         TTAAAAATGTCCTGCCTTTTAACGTAGATATAAGCCTTCCCCCACTACCGTAAATGTCCA
                                                                                                                                                                                                                  TITATATCATITITITATATATTCTTATAAAATGTAAAAAGAAAAACACCGCTTCTGCC
                                                                                                                                                                                                                                                                                           761 ITITCACTGIGITGGAGITITCIGGAGIGAGCACTCACGCCCTAAGCGCACAITCAIGIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEE: Venable, Baetjer, Howard & Civiletti, : 1201 New York Avenue, Suite 1000 Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/480,810
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: PCT/US95/03316
FILING DATE: 17-MAR-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 08/251,938 FILING DATE: 01-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US 08/215,086
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 36, Application US/09115252 Patent No. 6060301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Kamb, Alexander
TITLE OF INVENTION: MTS1 GENE
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 08
FILING DATE: 18-WAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08
FILING DATE: 14-APR-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 18-MAR-1
PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy
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STREET: 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: /note= "Splice site acceptor. US-09-120-130-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Splice site acceptor
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,369
FILING DATE: 14-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-MAR-1994
ATTORNEY/ACENT INFORMATION:
NAME: Inhen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24884-109348
TELEPHONE: 202-962-4810
TELEPHONE: 202-962-4810
                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 947 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature LOCATION: 458
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                                                                                                                                                                                                                                                                                                                                                                     linear
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                       ACAACTGCCCCCGCCACCACCCACCCGCTTTCGTAGTTTTCATTTAGAAAATAGAGCTT
                                                                                                                              701 ITTATATCATTTTTTATATATTCTTATAAAAATGTAAAAAGAAAAACACCGCTTCTGCC
                                                                                                                                                                                                                                                                              821 GGCATTICTIGCGAGCCTCGCAGCCTCCGGAAGCTGTCGACTTCATCACAAGCATTITGT
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                                                         TTAAAAATGTCCTGCCTTTTAACGTAGATATAAGCCTTCCCCCACTACCGTAAATGTCCA
   GENERAL INFORMATION:
APPLICANT: Beach, David
APPLICANT: Along, Yue
TITLE OF INVENTION: Cyclin Complex Rearrangement and
TITLE OF INVENTION: Related Thereto
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: ASCIITEM: C. DOS/MS. DOS SOFTWARE: ASCIITERX)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/154,915
FILING DATE: 19-NOV-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/991,997
FILING DATE: 17-DEC-1993
PROR APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-OCT-1993
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APPLICATION NUMBER: US 07/888,178
FILING DATE: 26-MAX-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/701,514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MII-026
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3: LAHIVE & COCKFIELD 60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/08154915
Patent No. 5618669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Vincent, Matthew P. REGISTRATION NUMBER: 36,7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 16-MAY-1993 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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(617) 227-5941
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US-08-154-915-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match 94.9%; Score 943.8; DB 5; Length 947; Best Local Similarity 99.8%; Pred. No. 3e-213; Matches 945; Conservative 0; Mismatches 2; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: /note= "Splice site acceptor." US-09-115-252-36
                                                                                                                                                                                                                                                                                                                                                                                                                                               "Splice site acceptor.
                                                                                                             24884-109348
                                                                     NAME: Ihhen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFRENCE/DOCKET NUMBER: 24884
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
INFORMATION FOR SEO ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 947 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: 151 OTHER INFORMATION: /note-
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 18-MAR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
NAME/KEY: misc_feature
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                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
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                                                                    Score 937.6; DB 6;
Pred. No. 8.6e-212;
0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-0CT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/991,997
FILING DATE: 17-DC-1992
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 948 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                           SULTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCI/US93/09945
FILING DATE:
                                                                                                                                                  Sequence 3, Application PC/TUS9309945 GENERAL INFORMATION:
                                                                                                                                                                                                                                COMPUTER: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-SOFTWARE: ASCTT**
                                                                                                                                                                           APPLICANT:
TITLE OF INVENTION: Cyclin Cor
TITLE OF INVENTION: Thereto
NUMBER OF SEQUENCES: 4
COMPUTER READABLE FORM:
MEDIUM IYPE: Floppy disk
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Best Local Similarity 99.6
Matches 940; Conservative
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19..465
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; LOCATION:
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PCT-US93-09945-3
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Pred. No. 8.6e-212;
0; Mismatches 4;
                                                                                                                                                                        94.3%; S
milarity 99.6%; P
Conservative 0;
        SEQUENCE CHARACTERISTICS:
LENGTH: 948 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
INFORMATION FOR SEQ ID NO:
                                                                                                         CDS
19..465
                                                                                                                                                                          Query Match
Best Local Similarity
Matches 940; Conserv
                                                                                                       NAME/KEY:

LOCATION:

US-08-154-915-3
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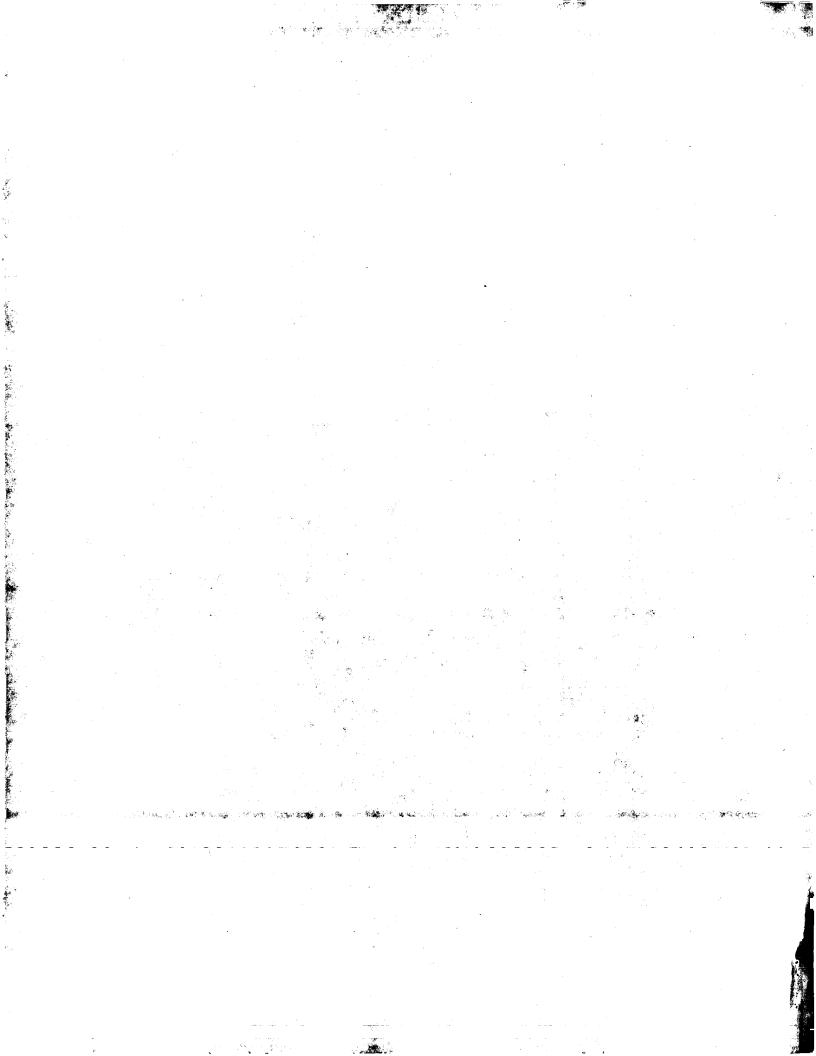
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Maximum Match 100%
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                                    OM nucleic - nucleic search, using sw model
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A18370819 w177d11.x
A1852049 9739507.x
A13822049 9739507.x
A138233 9155612.x
A1817709 w255112.x
A1817709 w256112.x
A1855096 w148b08.x
A1565096 w148b08.x
A1633790 tt28e10.x
A1863362 w1956403.x
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Matches 678; Conservative
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ORIGIN
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tb98f09.xl NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:2062409 3'
similar to SW:CDN2_HÜMAN P42771 CYCLIN-DEPENDENT KINASE 4 INHIBITOR
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qi40a06.x
nm88d08.s
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nr07f06.s
oq49e06.s
wf15a09.x
qd30a08.x
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wk89c11.x
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UI-R-BT0-
                                                                                                  ow59g04.x
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RESULT 1 AI337358/c LOCUS DEFINITION

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Onpublished (1997)
On Apr 7, 1998 this sequence version replaced gi:3036732.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert-Strausbergenh.gov
Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck,
M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
CLONG distribution: NOTI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LIMIL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1023 Std Error: 0.00
Seg primer: -40UP from Gibco
High quality sequence stop: 469.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Anote—Dorgan: colon; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA from the normalized library NCI_CGAP_CO10 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDS 1057416-1061255, and 114484-1145351).

Subtraction by Bento Scares and M. Fatima Bonaldo. "
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                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 689)
                                                                                                                                                                                                 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65.6%; Score 652.4; DB 38; Length 689; 98.4%; Pred. No. 6.8e-149; Live 0; Mismatches 9; Indels 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="IMAGE:2062409"
/clone_lib="NCI_CGAP_CO16"
/tissue_type="colon tumor, RER+"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
AI337358
AI337358.1 GI:4074285
                                                                                                        Homo sapiens
                                                                           human.
                          VERSION
KEYWORDS
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AW664294 568 bp mRNA EST 06-APR-2000 h109c04.x1 NCI_CGAP_GUI Homo sapiens cDNA clone IMACE:2971782 3' similar to TR:Q16361 Q16361 CELL CYCLE NEGATIVE REGULATOR BETA FORM
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                                                                                                                                                                    331 GCACCGGGCCGGGGGCGCGGCTGGACGTGCGCGATGCCTGGGGCCCGTCTGCCCGTGGACCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          691 TAAATGTCCATTTATATCATTTTTTATATATTGTTAAAAATGTAAAAAGACAC
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                                                                                                   679;
consisted of I.M.A.G.E. clones 260232-265223, 340488-345479, and 484488-489479." 154 c 178 g 182 t 7 others
                                                                                                     Length
                                                                                                                                    Indels
                                                                                                 Score 625.2; DB 38;
Pred. No. 2.9e-142;
0; Mismatches 19;
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                                                                                                 cch 62.9%;
11 Similarity 97.0%;
644; Conservative
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Eukaryota; Metazoa; C
Mammalia; Eutheria; P
1 (bases 1 to 568)
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A1379336 679 bp mRNA EST 25-JAN-1999 tc73g03.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:2070292 3' similar to TR:Q16361 Q16361 CELL CYCLE NEGATIVE REGULATOR BETA
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Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2070292"
/clone_lib="Soares_NhHMPu_S1"
/tissue_type="Pooled human melanocyte, fetal heart, and pregnant uterus"
/lab_host="PolloB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tumor Gene Index
Unpublished (1997)
On Dec 5, 1997 this sequence version replaced gi:2662837.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausbergfah, gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -40UP from Gloco
High quality sequence stop: 423.
Location/Qualiflers
1. 679
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                                                             894 TCAGGGGGTTACTGCTTCTTTGAGTCACACTGCTAGCAAATGGCAGAACCAAAGCTC
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               GGAGTTTTCTGGAGTGAGCACTCACGCCCTAAGCGCACATTCATGTGGGCCATTTCTTGCG
 CCACCACCCACCCCGCTTTCGTAGTTTTTTAGAAAATAGAGCTTTTAAAAATGTCCT
                                                                                                                                                                                                                   Homo sapiens
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata
Bummalia; Eutheria; Primates; Catarrhini; Hominida
1 (bases 1 to 679)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute; Cancer Genome Anatomy
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290 GACGCTGCCCGGGAGGGCTTCCTGGACACGCTGGTGCTGCACCGGGCCGGGGCGCGG 349
   88 AGGGGGGTTACTGGCTTCTCTTGAGTCACACTGCTAGCAAATGGCAGAACCAAAGCTCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 56.2%; Score 558.6; DB 39;
99.1%; Pred. No. 4.8e-126;
tive 0; Mismatches 5;
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                                 956 ATAAAAATAAAATTATTTTCATTC 983
                                                 28 ATAAAAATAAAATAATTTTCATTCATTC 1
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                                                         On Jul 7, 1999 this sequence version replaced gi:5407043.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550

Email: Robert Strausbergenih.gov
Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael R.
Email: Robert Strausbergenih.gov
Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D., CDNA Library Preparation: Life
Technologies, Inc. CONA Library Arrayed by: Christa Prange,
Technologies, Inc. Consortium DNA Sequencing by: Washington University
Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/Library at:
Image.llni.gov/Anage/Atml/Airesources.shtml
Seq primer: -40UP from Gibco
High quality sequence stop: 417.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        /note-"Organ: genitourinary tract; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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/tissue_type="2 pooled high-grade transitional cell
tumors"
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/clone="IMAGE:2971782"
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AUTHORS
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Tunor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

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Tel: (301) 496-1560

Tel: (301) 496-1560

Tel: (301) 496-1560

Tissue Procurement: Ash Alizadeh, John Byrd, M.D., Mike Grever,

M.D., Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Parayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image.html

Insert Length: 755 Std Error: 0.00

Seq primer: -400P from Gibco

High quality sequence stop: 457.

Location/Qualifiers

Li.: 566/Gualifiers

Lirce

Li.: 566/Gualifiers
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
/tissue_type="anaplastic oligodendroglioma"
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I (bases 1 to 590)

National Cancer institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAPTBTAB); Tumor Gene Index

Unpublished (1998)

On Oct 30, 1998 this sequence version replaced gi:3813427.

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert_Strausberg@aih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing Dy: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.lnl.gov/bbrp/image/image.html
Insert Length: 845 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 444.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A1871381 590 bp mRNA EST 07-MAR-2000 w181d11.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2431317 3' similar to TR:016361 016361 CELL CYCLE NEGATIVE REGULATOR BETA FORM 7', mRNA sequence.

A1871381 GI:5545430
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                                                                                                                                                                                                                                                                                                                                                       Email: Robert_Strausberg@nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld
CCCGCCACAACCCACCCCCCTTCGTAGTTTTCATTTAGAAATAGAGCTTTTAAAAATG
                                                          146 CCCGCCACACCCACCCCGCTTTCGTAGTTTTAGAAATAGAGCTTTTAAAATG
                                            CTGGACGTGCGCGATGCCTGGGGCCGTCTGCCCGTGGACCTGGCTGAGGACCTGGGCCAT
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AUTHORS
TITLE
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w177d11.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2430933 3' similar to TR:016361 Q16361 CELL CYCLE NEGATIVE REGULATOR BETA FORM 7, mRNA sequence.
A1870879.1 G1:5544847
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                                                                                                                                                                        Length 590;
                                                                                                                                                                        Score 558.2; DB 45; Length
Pred. No. 6e-126;
0; Mismatches 3; Indels
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
Tumor Gene Index
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert Strausberg@nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Email: Robert Strausberg@nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emart-Buck, M.D., Ph.D.
CDNA Library Prayaration: Life Technologies, Inc.
CDNA Library Narayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1276 Std Error: 0.00
Seq primer: -400P from Gibco.
                                                                                                                                                                                                                                                                                                                                                                                   ALESYB22 604 bp mRNA EST 07-MAR-2000 wm20h06.xl NCI_CGAP_Ut4 Homo sapiens cDNA clone IMAGE:2436539 3' similar to TR:Q16361 Q16361 CELL CYCLE NEGATIVE REGULATOR BETA FORM 1, MRNA sequence.
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Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.48 kb. Life Technologies catalog #:
11542-016"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 604)
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/clone_lib="NCI_CGAP_Ut4"
/tissue_type="serous papillary carcinoma, high grade, pooled tumors"
                                                                                                                                              196 TTAGATCATCAGTCACCGAAGGTCCTACAGGGCCACAACTGCCCCCGCCACAACCCCACCC 137
                                                                                                   136 CGCTTTCGTAGTTTTCATTTAGAAATAGAGCTTTTAAAAATGTCCTGCCTTTTAACGTA 77
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DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
Gound through the I.M.A.G.E. Consortium/LLNL at:
Insert Length: 819 Std Error: 0.00
Seq primer: -400P from Glbco
High quality sequence stop: 474.
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                                                                                                                                                                                                                   Email: Robert_Strausberg@nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index Unpublished (1998)
On May 18, 1998 this sequence version replaced gi:3136859.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
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98.9%; Pred. No. 4.5e-123;
iive ,0; Mismatches 6;
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Matches 550; Conservative
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AI198233 579 bp mRNA EST 02-DEC-1998
q155d12.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:1860407 3'
similar to TR:Q16361 Q16361 CELL CYCLE NEGATIVE REGULATOR BETA FORM
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Pred. No. 1.5e-122;
O; Mismatches 8; Indels
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/lab_host="Bh108"
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                             Location/Qualifiers
-40UP from Gibco
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Local Similarity 98.6%;
les 549; Conservative
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CDNA Library Parayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
Www.bio.llnl.gov/bbrp/image/image.html
Insert Length: 884 Std Error: 0.00
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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NCI/NINDS-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NCI/NINDS-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NCI/NINDS-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.

Orational forcer institute Antional Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BFGAP), Tumor Gene Index

Onpublished (1998)

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Email: Robert_Strausberg@nih.gov
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                TAGAAAATAGAGCTTTTAAAAATGTCCTGCCTTTTAACGTAGATATAAGCCTTCCCCCAC
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                                                                               TACCGTAAATGTCCATTTATATCATTTTTTATATATTCTTATAAAAATGTAAAAAAGAAA
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Tissue Procurement: David N. Louis, M.D., Myrna
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AI362049.1 GI:4113670
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Bonaldo, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

CDNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CBP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:

www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 729 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 459.

Location/Qualifiers
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                                                                                                                                                                                                                                                                     Email: Robert_Strausberg@nih.gov
Lissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
I (bases 1 to 579; //www.ncbi.nlm.nih.gov/ncicgap.
NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurological Stockes, Brain Tumor Genome Anatomy Project (CGAP/PBTGAP), Tumor Gene Index
;, mRNA sequence.
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                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
                                AI198233.1 GI:3750839
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Matches 548; Conservative
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

Eu (Abases 1 to 729)

NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index

(CGAP/BTGAP), Tumor Gene Index

On Apr 7, 1998 this sequence version replaced gi:3035534.

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert_Strausbergeihh.gov

Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             A1817709 729 bp mRNA EST 21-DEC-1999 wk25c11.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2413364 3' similar to TR:Q13399 Q13399 HYPOTHETICAL 18.1 KDA PROTEIN ;, mRNA
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488 GGTCCCTCAGACATCCCCGGATTGAAAGAACCAGAGGCTCTGAGAAACCTCGGGAAACT
                                                                               /clone="IMAGE:2413364"
/clone_lib="NCI_CGAP_Brn25"
/tissue_type="anaplastic oligodendroglioma"
/lab_host="DH10B"
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Insert Length: 848 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 468.
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/db_xref="taxon:9606"
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Sequencing Center information can be

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/ Indage:"Pactor: pT773D-Pac (Pharmacia) with a modified
polylinker: Plasmid DNA from the normalized library
NOI. CGAP_GC4 was prepared, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified CDNAs from a pool of 5,000 clones made
from the same library (cloneIDs 1257096-1258631,
1469064-1470993, and 1475992-1476743). Subtraction by
Bento Soares and M. Fatima Bonaldo. "
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70 ATATECCTTCCCCCACTACCGTAAATGTCCATTTATATATCTTTTTTATATATTCTTATAAA
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CDNA Library Preparation: M. Bento Soares, Ph.D., M. Bonado, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 613 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 460.
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98.9%; Pred. No. 4.4e-119;
11ve 0; Mismatches 5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
mail: Robert_Strausberg@nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D.
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Pred. No. 2.8e-120;
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     M.Fatima
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al Similarity 98.7%;
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On Feb 22, 1999 this sequence version replaced gi:4283180.
On Feb 22, 1999 this sequence version replaced gi:4283180.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert-Strausberg@hih.gov. Michael R. Emmert-Buck,
M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
CLONE distribution: NOI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/Link at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 844 Std Error: 0.00
High quality sequence stop: 400.
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Subtraction by Bento Soares and M. Fatima Bonaldo. " a 220 c 221 g 179 t 1 others
                                                                                 AI765096 774 bp mRNA EST 21-DEC-1999 W4489B08.XI NOI_CGAP_CO16 HONG sapiens cDNA clone IMAGE:2293463 3' similar to TR:013399 Q13399 HYPOTHETICAL 18.1 KDA PROTEIN ;contains LTR9.b3 WER22 repetitive element ; mRNA sequence.
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                                                                                                                                                                                                                                          Euteleostomi;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 774)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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/db_xref="taxon:9606"
/dclone=lib="xrcl_CGAP_Co16"
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/lab_host="DH108"
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AI765096.1 GI:5231605
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Best Local S:
Matches 583
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LOCUS
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VERSION
KEYWORDS
SOURCE
ORGANISM
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ORIGIN
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El (bases 1 to 531)

I (bases 1 to 531)

NGI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

Unpublished (1997)

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Tel: (310) 496-1550

Email: Robert Strausbergenh.gov

Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.
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DNA Sequencing by: Washington University Genome Sequencing Conte.
Clone distribution: NCI-CGAP Clone distribution information can J
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/Dbrp/image/image.html
Insert Length: 623 Std Error: 0.00
seq primer: -400P from Gibco.
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Center n can be

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Bonaldo, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

Clone distribution: NCI-CGAP clone distribution information can l found through the I.M.A.G.E. Consortium/LLNL at:

Insert Length: 626 Std Error: 0.00

Seq prime: -400P from Gibco
                                                                                                               Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nlh.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.
NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurological
Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/BTGAP), Tumor Gene Index
Unpublished (1998)
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                                                                                                                                                                                                                                  cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
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/db_xref="taxon:9606"
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/lab_host="DH108"
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Pred. No. 2e-117;
0; Mismatches 3;
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Location/Qualifiers
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Kukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 528)
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AI885362
AI885362.1 GI:5590526
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Best Local Similarity
Matches 527; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.lnl.gov/bbrp/lmage/lmage.html
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High quality sequence stop: 462.
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143 c 163 g 114 t 2 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: Robert_Strausbergenih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 528).
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
635 GAGCTITIAAAAATGTCCTGCCTTTTAACGTAGATATAAGCCTTCCCCCACTACCGTAAA 694
                      Tumor Gene Index
Tumor Gene Index
Unpublished (1997)
On Apr 7, 1998 this sequence version replaced gi:3036438.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Bmail: Robert_Strausbergenth any
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Search completed: July 21, 2000, 02:48:40 Job time: 9635 sec

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212 CGAGTGGCGGAGCTGCTGCTCCTCGCGCGCGGAGCCCAACTGCGCCCGACCCCGCCACT 271

Best_Local Similarity 99.2 Matches 524; Conservative

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AR001314 Sequence 1 from patent
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AR062774 Sequence 1 from patent
                                                                                                                                                           About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
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AR062774
                                                                                                                                                         1 (bases 1 to 471)
Stone, S., Jiang, P. and Kamb, A.
Mouse MTSI gene
Patent: 18 5843756-A 1 01-DEC-
Location/Qualifiers
                                                                                                                                                                                                                          /organism="unknown"
153 c 186 g
                                                                                                                                                                                                                                                                                                                                                                           from: 1
                                                                                                     AR062774.1 GI:5990465
                                                                    471 bp
              468
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5.090
99.359
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LOCUS AR062774
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Unclassified
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Ratio:
Percent Similarity:
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VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                   source
                                                                              DEFINITION
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ORIGIN
                                                                                                                                                         REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                      FEATURES
                                                                                                                                                                   1 (bases 1 to 471)
Kamb, A.
Probes for WTS1 gene and polynucleotides encoding mutant MTS1 genes
Patent: US 5801236 A 1 01-SEP-1998;
Location/Qualifiers
                                                                              29-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GlyAlaArgLeuAspValArgAspAlaTrpGlyArgLeuProValAspLe 117
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                                                                              PAT
                                                                                                                                                                                                                                                                                                      Length: 156
Gaps: 0
Percent Identity: 98.718
                                                                                                                                                                                                                                                  64
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AR037494
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153 c 186 q
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                                                                                                                                                                                                                                                                                                                                                                                    from: 1
151 ProSerAspIleProAsp 156
                     451 CCCTCAGACATCCCCGAT 468
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5.090
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US-09-016-869A-2 x AR037494
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JS AR037494
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Quality:
Ratio:
Percent Similarity:
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                                                                                        DEFINITION
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FEATURES
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source

JOURNAL FEATURES

BASE COUNT

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ORGANISM

ACCESSION VERSION KEYWORDS

AUTHORS TITLE

REFERENCE

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84 spalaalaargGluGlyPheLeuAspThrLeuValValLeuHisArgAla 100
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                                                                                                                                                                                                                                                                                                                                                     ValMetMetMetGlySerAlaArgValAlaGluLeuLeuLeuHisGl
                                                                                                                                                                                                                                               Length: 156
Gaps: 0
Percent Identity: 98.718
                                         PAT
                                                                                                                      1 (bases 1 to 947)
Kamb.A.
Warshel. beta. gene
Patent: US 5739027-A 36 14-APR-1998;
                                                                                                                                                                                              195
                                                  5739027
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                                                                                                                                                                Location/Qualifiers 1. 947
                                                                                                                                                                                  /organism="unknown"
271 c 274 g
                                                  as
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                                       AR001346 947 bp
Sequence 36 from patent
AR001346
                                                                   AR001346.1 GI:3963413
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Quality:
Ratio:
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                                                                                                       Unclassified.

I (bases 1 to 471)

Skolinick, M. H., Cannon Albright, L.A. and Kamb, A. Germline mutations in the MTS gene
AL Patent: US 5624819-A 1 29-APR-1997;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GlyalaArgLeuAspValArgAspAlaTrpGlyArgLeuProValAspLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          301 GGGGCGCGCTGGACGTGCGCGATGCCTGGGGCCGTCTGCCCGTGGACCT
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Gaps: 0
Percent Identity: 98.718
                                                   PAT
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LOCUS 141148 471 bp DNA
DEFINITION Sequence 1 from patent US 5624819.
CESSION 141148.1 GI:2081738
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153 c 186 g
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451 CCCTCAGACATCCCCGAT
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US-09-016-869A-2 x I41148
                   seq_name: gb_pat:141148
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151

351

117

us-09-016-869a-2.rge

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Locus AR062806
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Ratio:
Percent Similarity:
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                                                                                                                                                                                                      ORIGIN
                                                                                                                       1 (bases 1 to 947)
Kamb, A.
Probes for MTS1 gene and polynucleotides encoding mutant MTS1 genes
Patent: US 5801236-A 36 01-5EP-1998;
                                 29-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  uAlaGluGluLeuGlyHisArgAspValAlaArgTyrLeuArgAlaAlaA 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        101 CGGGGCGCTGCCCAACGCACCGAATAGTTACGGTCGGAGGCCGATCCAG 150
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Gaps: 0
Percent Identity: 98.718
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US 5801236.
                                                                                                                                                                   Location/Qualifiers
1. .947
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271 c 274 g
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LOCUS AR037526 947 bp DEFINITION Sequence 36 from patent ARCESSION AR037526 GI:5955382
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US-09-016-869A-2 x AR037526
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Percent Similarity:
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                                                                             KEYWORDS
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                                                                                                                                                                                                                              Length: 156
Gaps: 0
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                                                                                        1 (bases 1 to 947)
Stone,S., Jlang,P. and Kamb,A.
Mouse MTSI gene
Patent: US 5843756-A 36 01-DEC-1998;
           5843756
                                                                                                                                                                        195
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                                                                                                                                       Location/Qualifiers 1. .947
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947 bp
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20-MAR-1996

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COMMENT
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           13-MAY-1997
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                                                                                                                                                                                                                                                                                                                                    1 MetAspProAlaAlaGlySerSerMetGluProSerAlaAspTrpLeuAl 17
                                                                           Unknown.
Unclassified.
1 (bases 1 to 947)
Skollick, M. H., Cannon-Albright, L.A. and Kamb, A.
Germline mutations in the MTS gene
Patent: US 5624819-A 36 29-APR-1997;
                                                                                                                                                                                                                                  Length: 156
Gaps: 0
Percent Identity: 98.718
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   141180 947 bp DNA
Sequence 36 from patent US 5624819.
141180
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271 c 274 g
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VERSION
KEYWORDS
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JOURNAL
FEATURES
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                                                                                                                                                                                                                                                          2 (bases 1 to 987)
Okamoto,A., Demetrick,D.J., Spillare,E.A., Hagiwara,K.,
Hussain,S.P., Bennett,W.P., Forrester,K., Gerwin,B., Serrano,M.
Beach,D.H. and Harris,C.C.
Mutations and altered expression of p16INK4 in human cancer
Proc. Natl. Acad. Sci. U.S.A. 91 (23), 11045-11049 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (02-JAN-1994) Manuel Serrano, Cold Spring Harbor
Laboratory, 1 Bungtown Road, Cold Spring Harbor, NY 11724, USA
4 (bases 1 to 987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
                                                                                                         Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 60 to 987)
Serrano,M., Hannon,G.J. and Beach,D.
A new regulatory motif in cell-cycle control causing specific inhibition of cyclin D/CDK4
Nature 366 (6456), 704-707 (1993)
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Submitted (01-SEP-1994) Manuel Serrano, Cold Spring Harbor
Laboratory, 1 Bungtown Road, Cold Spring Harbor, NY 11724, I
On Oct 18, 1994 this sequence version replaced gi:535942.
mRNA PRI 2
(p16-INK4) mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length: 156
Gaps: 0
Percent Identity: 98.718
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a 279 c 295 g 1
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 HUMINK4X 987 bp
Human CDK4-inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                              (bases 60 to 987)
                                       L27211
L27211.1 GI:558656
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
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US-09-016-869A-2 x HUMINK4X
                                                                        CDK4; cyclin D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Serrano, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ø
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Ratio:
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                                                                                               human.
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84

67

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Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 793)

Robertson, K.D. and Jones, P.A.

Tissue-specific alternative splicing in the human INK4a/ARF cell

cycle regulatory locus

Orocene (1998) In press

E (bases 1 to 793)

KS Robertson, K.D. and Jones, P.A.

Direct Submission

Ni Submitted (21-DEC-1998) Cancer Center, University of Southern

California, 1441 Eastlake Ave. MS 73, Los Angeles, CA 90033, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens cyclin-dependent kinase inhibitor pl2 (pl6INK4a) mRNA, alternatively spliced form, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="cyclin-dependent kinase inhibitor p12"
/protein_id="AAD11437.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="alternatively spliced form of p16INK4a" /codon_start=1
                                                                                                                                                                                                                                                                                                           1109 CGGGGGGCACCAGAGGCAGTAACCATGCCCGCATAGATGCCGCGGAAGGT 1158
                                                                                                                                                                                                                                             84 spalaalaargGluGlyPheLeuAspThrLeuValValLeuHisArgAla 100
                                                                                                                                                                                                                                                                                                                                                                                                                                         134 laGlyGlyThrArgGlySerAsnHisAlaArgIleAspAlaAlaGluGly 150
                                                                                                                                 '59 CACGCCCCCCCCCCCGGGTCGGGTAGAGGAGGTGCCGGGCCGCTGCTGGAGG
                                                                                                                                                                                67 yAlaGluProAsnCysAlaAspProAlaThrLeuThrArgProValHisA
                                                                                                                51 ValMetMetMetGlySerAlaArgValAlaGluLeuLeuLeuHisGl
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/chromosome="9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="pancreas"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
1. .793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="p16INK4a"
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AF115544.1 GI:4206166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1159 CCCTCAGACATCCCCGAT 1176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_name: gb_pr4:AF115544
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LOCUS AF115544
DEFINITION Homo sapiens
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Unknown.
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Unclassified.
Unclassified.
Gyuzis, J. tamphere, L. and Beach, D.
Gyuzis, J. so cell-cycle progression, and uses related thereto Inhbitors of cell-cycle progression, and uses related thereto Patent: US 5672508-A 1 30-SEP-1997;
Location/Qualifiers
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134 laGlyGlyThrArgGlySerAsnHisAlaArgIleAspAlaAlaGluGly 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       spAlaAlaArgGluGlyPheLeuAspThrLeuValValLeuHisArgAla 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17 aThralaAlaAlaArgGlyArgValGluGluValArgAlaLeuLeuGluA 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PAT
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Gaps: 0
Percent Identity: 98.718
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Sequence 1 from patent US 56
167718 1G:2731253
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LOCUS 167718
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SOURCE

REFERENCE AUTHORS

DEFINITION

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84

ACCESSION VERSION KEYWORDS

source

TITLE JOURNAL FEATURES

BASE COUNT ORIGIN

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alignment_block:
US-09-016-869A-2 x HSU26727
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             451 GGCGGAGCTGCTGCTGCTCCACGCGCGGAGCCCAACTGCGCCGACCCCG 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       101 cGGGGGCGCTGCCCAACGCACGAATAGTTACGGTCGGAGGCCGATCCAG 150
                                                                                                                                                                                                                                                                                                                                                                                                            201 GACGAAGTTTGCAGGGGAATTGGAATCAGGTAGCGCTTCGATTCTCCGGA 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               251 AAAAGGGGAGGCTTCCTGGGGAGTTTTCAGAAGGGGTTTGTAATCACAGA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 351 AGGAGCCACGCGCGTACAGATCTCTCGAATGCTGAGAAGATCTGAAGGGG 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                301 CCTCCTCCTGGCGACGCCCTGGGGGCTTGGGAAACCAAGGAAGAGGAATG 350
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                                                                                                                                                                                                                                                                                                                               34 laValAlaLeuProAsnAlaProAsnSerTyrGlyArgArgProile.Gl 50
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                                                                                                                                                                                                                                                     Length: 248
Gaps: 2
Percent Identity: 61.694
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                                                 300 g
                                   PGDALGAWETKEEE'
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4.623
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                                                                                                                Quality:
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LVLMLLRSQRLGQQPLPRRPGHDDGQRPSGGAAAAPRRGAQLRRPRHSHPTRARRCPG
GLPGHAGGAAPGRGAAGRARCLGPSARGPG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="also called exon 0.18, substituted by alternative splicing to pl61NK4 exon 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (10-MAY-1995) Christian-Jacques Larsen, Institut de
Genetique moleculaire, U-301 Inserm, 27, rue juliette Dodu, Paris
                                                                                                                                                                                                                                                                                                                                  buro,D., Bernard,O., Della Valle,V., Berger,R. and Larsen,C.J.
A new type of pl6INK4/MTS1 gene transcript expressed in B-cell
malignancies
                                                                                                                                              30-NOV-1995
                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to index)
Duro, D., Bernard,O., Della Valle,V., Berger,R. and Larsen,C.J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="pl6INK4/MTS1"
28. 426
/note="pl6INK4/MTS1"
/note="a frameshift between exon 1 (0.18) and exon changed the ORF of pl6INK4 gene."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length: 174
Gaps: 2
Percent Identity: 66.092
                                                                                                                                                 PRI
HSU26727 1017 bp mRNA
Human p16INK4/MTS1 mRNA, complete cds.
U26727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /cell_line="RPMI 8226"
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/tissue_type="hematopoietic"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /protein_id="AAA82236.1"
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/chromosome="9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     528. .1017
/gene="p16INK4/MTS1"
/number=3
a 297 c 291 g
                                                                                                                                                                                                                                                                                                                                                                                                                  Oncogene 11 (1), 21-29 (1995) 95349933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene-"pl6INK4/MTS1"
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1. .1017
                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 (bases 1 to 1017)
Larsen, C.-J.
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                                                                                                                                                                                                         U26727.1 GI:862412
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4.358
72.989
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                                                                                    seq_name: gb_pr2:HSU26727
                                                                                                                         seq_documentation_block:
                                                                                                                                                                                                                                                                        Homo sapiens
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Ratio:
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125 49 20

83

317 66 367 116 417 133 467 149

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//d_xxef="c1:1000572"
//tanslationslations
AREGFLDTLVVIHRAGARLDVRDAMGRLPVDLAEELGHRDVARYIRAAAGGTRGSNHA
                                                                                                                                                                                                                                                                                                                                                            form; This
translation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     531
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                                                                                                                                                                                                                                               /gene="P16/MTS1/CDKN2"
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308. .655
                                                                                                                                                                                                                                                                                                                                                            regulator beta
; Stop to stop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              116 pLeuAlaGluGluLeuGlyHisArgAspValAlaArgTyrLeuArgAlaA 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66
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                                                                         13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   482 GCCGGGGCGCGCGCTGGACGTGCCTGGGGCCGTCTGCCGTGGA
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Gaps: 0
Percent Identity: 100.000
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                                                                           from
                                                       /gene="tumor suppressor gene"
/note="This sequence comes fr
                                                                                                                                                                                                                                                                                                                                                          /note="cell cycle negative resequence comes from Fig. 1B;
                   /gene="tumor suppressor gene'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              u
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66
                                                                                                          /protein_id="AAC60649.1"
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                                                                                                                                                                                                                                                                                               308, .655
/partial
/gene="P16/MTS1/CDKN2"
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/partial
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Percent Similarity: 100.000
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US-09-016-869A-2 x S78535
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P16/MTS1/CDKN2=cell cycle negative regulator
Partial, 660 nt].
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 660)

Stone, S., Jiang, P., Dayananth, P., Tavtigian, S.V., Katcher, H., Parry, D., Peters, G. and Kamb, A.

Complex structure and regulation of the P16 (MTS1) locus
Cancer Res. 55 (14), 2988-2994 (1995)
                                                                                                                                                  GCGCGTGCGCCCCCCCGCGAGTGAGGGTTTTCGTGGTTCACATCCCCCCG 114
                                                                                                                                                                                                                                         ......AGTGGGCAGCGCCAGGGGCGCCCGCCGCTGTGGCCCTCGTGC 166
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             to: HSU26727 from: 1
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beta form [human, mRNA
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S78535.1 GI:1000570
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KEYWORDS

REFERENCE AUTHORS

TITLE JOURNAL

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Probes for MTS1 gene and polynucleotides encoding mutant MTS1 genes
Patent: US 5801236-A 13 01-SEP-1998;
Location/Qualifiers
1. .1131
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MTS1E1.beta. gene
Patent: US 5739027-A 13 14-APR-1998;
Patent: UCation/Qualifiers
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Sequence 13 from patent US 5739027.
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Ratio: 5.168
Percent Similarity: 100.000
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116 pLeuAlaGluGluLeuGlyHisArgAspValAlaArgTyrLeuArgAlaA 133
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Percent Identity: 100.000
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 N_Geneseq_36:099165
N_Geneseq_36:T69781
N_Geneseq_36:V11250
N_Geneseq_36:V53831
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Human multiple tumour suppress
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Multiple tumour suppressor 1
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                                                                                                                                  About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
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OM of: US-09-016-869A-2 to: N_Geneseq_36:*
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Query: US-09-016-869A-2
Query length: 156
Database: N_Geneseq_36:*
Database sequences: 311585
Database length: 125096042
Search time (sec): 109.050000
                                Date: Jul 21, 2000 9:30
                                                                                                                        Command line parameters:
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N_Genesed_36:100750
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N_Geneseq_36:V112311
N_Geneseq_36:V53851
N_Geneseq_36:V50615
N_Geneseq_36:V50615
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N_Geneseq_36:V53821
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Sequence
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Human multiple tumour suppre
Human multiple tumour suppre
Human MTS2 cDNA. DNA specifi
Coding sequence 2 of the mul
                                                                                                                                                                                                                                       Cell-cycle regulatory protein p16 cDNA.
Cell-cycle regulatory protein p16; cyclin-dependent kinase inhibitor;
CCR; gene therapy; transgenic animal; cancer; cell proliferation;
SS; d8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New cell cycle regulating proteins bind to cyclin dependent kinase and related nucleic acids, antibodies etc., used in diagnosis and the related nucleic acids, antibodies etc., used in diagnosis and the abnormal cell proliferation, degeneration etc.

Claim 43: Page 76-77: 109pp: English.

CDNA (102962) coding for the human cell-cycle regulatory (CCR) protein p16 (R85116) was isolated using a 2-hybrid screening assay in Saccharomyces cerevisiae. The p16 gene was mapped to chromosome 9pp1-22. The isolated cDNA can be used: to detect mutations in CCR genes that lead to cell proliferation; to breed transgenic animals to study cellular disorders involving CCR allele mutation/misexpression; and to correct CCR deficient cells (gene therapy).
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14-APR-1994; US-227371.
14-SEP-1994; US-248812.
14-SEP-1994; US-346147.
29-NOV-1994; US-346147.
(COLD-) COLD SPRING HARBOR LA
Beach DH, Demetrick DJ, Han
WPI; 95-373798/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               225 A;
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Ratio: 5.128
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151

491

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MTS1; multiple tumour suppressor; diagnosis; cancer; germ-line mutation; familial melanoma locus; MIM; predisposition; ds.
                                                                                                                                                                 DNA specific for Multiple Tumour Suppressor 1E1-beta gene useful for the diagnosis of cancers related to MTS1E1-beta
                                                                                                                                   51 CACGGCGCGCGCGCGCGGTCGGGTAGAGGAGGTGCGGGGCGCTGCTGGAGG 100
                                                                                                                                                                                                                                                                                                                                                                       84 spalaalaargGluGlyPheLeuAspThrLeuValValLeuHisArgAla 100
                                                                                                                                                                                                                                                                                                                                                                                                                                        ualaGluGluLeuGlyHisArgAspValalaArgTyrLeuArgAlaAlaA 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17 aThralaalaalaargGlyargValGluGluValArgAlaLeuLeuGluA
                                                                                                                                                                                                                                                                                                                                                                                         1 MetAspProAlaAlaGlySerSerMetGluProSerAlaAspTrpLeuAl
                                                    67 yAlaGluProAsnCysAlaAspProAlaThrLeuThrArgProValHisA
                                                                                                                                                                                                                                                                                                                                        201 GCGGAGCCCAACTGCGCCGACCCGCCACTCTCACCCGACCCGTGCACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          301 GGGGCGCGGCTGGACGTGCGCGATGCCTGGGGGCCGTCTGCCCGTGGACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "multiple tumour suppressor"
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د
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag= a
/product= MTS1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_documentation_block:
ID V11238 standard; cDNA; 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             151 ProSerAspileProAsp 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             451 CCCTCAGACATCCCCGAT 468
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_name: N_Geneseq_36:V11238
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18-MAR-1994; US-215086.

18-MAR-1994; US-227369.

01-UNN 1994; US-227369.

17-MAR-1995; WO-U03316.
to: T00747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 98-250421/22.
P-PSDB; W40524.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human MTS1 cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US5739027-A
Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                V11238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kamb A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Detecting polymorphism associated with cancer pre:disposition - also DNA, vectors and host cells e.g. for gene or protein replacement therapy and drug screening Dlsclosure; Pages 111-121; 148pp; English. An individual can be diagnosed as having a predisposition to cancer by detecting an alteration in the wild type multiple tumour suppressor (MTS) gene, using gene probes which hybridise to the MTSI prognosis of melanoma, lymphoma, leukaemia and pancreas, breast and
                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-MXY-1996 (first entry)
Multiple tumour suppressor 1 (MTS1) cDNA.
Multiple tumour suppressor; MTS1; cancer; diagnosis; assay;
predisposition; melanoma; leukaemia; lymphoma; prognosis;
pancreas; breast; thyroid; ds.
                               241 CCCGGAGCCCAACTGCGCCGACCCCGCCACTCTCACCCGACCCGTGCACG 290
                                                                                                  GlyalaArgLeuAspValArgAspAlaTrpGlyArgLeuProValAspLe 117
                                                                                                                                   GGGCGCCGCTGGACGTGCGCGATGCCTGGGGCCGTCTGCCCGTGGACCT 390
                                                                                                                                                                                   Ë
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         196
                                                                                                                                                                   uAlaGluGluLeuGlyHisArgAspValAlaArgTyrLeuArgAlaAlaA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length: 156
Gaps: 0
Percent Identity: 99.359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ΰ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= a
/note= "splice site acceptor"
458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= b
/note= "splice site acceptor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kamb A, Skolnick MH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         271 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                       T00747 standard; cDNA; 947 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-MAR-1994; US-214582.

18-MAR-1994; US-215087.

18-MAR-1994; US-215086.

14-APR-1994; US-227369.

01-JUN-1994; US-251938.

(MYRI-) MYRIAD GENETICS INC.

(UTAH) UNIV UTAH RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        207 A;
                                                                                                                                                                                                                                                                                                      ProSerAspileProAsp 156
                                                                                                                                                                                                                                                                                                                                        CCCTCAGACATCCCCGAT 508
                                                                                                                                                                                                                                                                                                                                                                       seg_name: N_Geneseg_36:T00747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality: 796.00
Ratio: 5.103
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cancers, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_block:
US-09-016-869A-2 x T00747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cannon-Albright LA,
WPI; 95-344626/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9525813-A1.
28-SEP-1995.
17-MAR-1995; U03537.
                                                                                                                                                                                                                                                                                                                                                                                                         documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             misc_feature
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alignment_scores

Sequence thyroid

250

84

300

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This is the nucleotide sequence of the multiple tumour suppressor I
This is the nucleotide sequence of the multiple tumour suppressor I
(MTS-1) gene, used in the method of the invention. The MTS gene
is useful in the diagnosis and prognosis of human cancer, e.g. by
standard nucleic hybridisation techniques, of patient samples. The
mutated sequences are those that are present in somatic mutations
of the gene in cancers. The vectors can be used for gene therapy
strategies to replace function of mutated protein in patients. These
can also be used to construct protein minetics, also for therappeutic
strategies. In addition the expression constructs can also be used
for recombinant production of MTS. Recombinant MTS can be used to
conserve in addition the expression constructs can also be used
for recombinant production of MTS. Recombinant MTS can be used to
conserve in addition the sectore MTS function in a cell.
Itself may also be used to restore MTS function in a cell.
                                                                                                                                                                                                                                                                                                                                                    P-PSDB; W4549.
Nucleic acids based on multiple tumour suppressor, MTS, sequences useful as hybridisation probes, primers and recombinant production of MTS in the diagnosis and treatment of cancers related to MTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       201 CGCGGAGCCCAACTGCGCCCAACCCCGCCACTCTCACCCGACCCGTGCACG 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84 spAlaAlaArgGluGlyPheLeuAspThrLeuValValLeuHisArgAla 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             101 GlyalaArgLeuAspValArgAspAlaTrpGlyArgLeuProValAspLe 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  yAlaGluProAsnCysAlaAspProAlaThrLeuThrArgProValHisA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34 laValAlaLeuProAsnAlaProAsnSerTyrGlyArgArgProIleGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MetAspProAlaalaGlySerSerMetGluProSerAlaAspTrpLeuAl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51 ValMetMetMetGlySerAlaArgValAlaGluLeuLeuLeuHisGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length: 156
Gaps: 0
Percent Identity: 98.718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to: V53819 from: 1 to: 471
                                                                                                                                                                                18-MAR-1994; US-215086.

18-MAR-1994; US-215087.

14-APR-1994; US-227369.

01-UUN-1994; US-251938.

17-MAR-1995; WO-UO3316.

(MYRI-) MYRIAD GENETICS INC.
                               /*tag= a
/product=
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5.090
99.359
                                                                                                                                     US-480810.
US-214582.
         1. 471
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US-09-016-869A-2 x V53819
                                                                                                                                                                                                                                                                                                                                     98-494842/42.
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                                                                                                                                                           18-MAR-1994;
18-MAR-1994;
                                                                                                                                  07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                               mutation(s)
Claim 1; Co
                                                                                            01-SEP-1998
                                                                                                                                                                                                                                                                                                                   Kamb A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29
         CDS
         mutation(s) and their treatment
Disclosure; Column 61-62; 72pp; English.
This oDNA sequence encodes a human multiple tumour suppression protein,
MTS1. The MTS gene locus is also referred to as the familial melanoma
(MLM) gene locus, located on human chromosome 9p21. Germ line mutations
in MTS genes can be used in the diagnosis of predisposition to cancers,
e.g. melanoma, leukaemia, astrocytoma, gliboblastoma, lymphoma, glioma,
Hoddkin's lymphoma, CLL, and cancers of the pancreas, breast, thyroid,
ovary, uterus, testis, kidney, stomach and rectum.
Sequence 471 BP; 68 A; 153 C; 186 G; 64 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-DEC-1998 (first entry)
Nucleotide sequence of the CDS of the multiple tumour suppressor 1.
Multiple tumour suppressor 1; MTS-1; human; cancer; hybridisation; somatic mutation; gene therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            101 CGCGGAGCCCAACTGCGCCGACCCCGCCACTCTCACCCGACCCGTGCACG 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84 spalaalaargGluGlyPheLeuAspThrLeuValValLeuHisArgAla 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GlyAlaargLeuAspValargAspAlaTrpGlyArgLeuProValAspLe 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       101 CGGGGGCGCTGCCCAACGCACCGAATAGTTACGGTCGGAGGCCGATCCAG 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             151 GTCATGATGATGGGCAGCGCCGAGTGGCGGAGCTGCTGCTGCTCCACGG 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51 CACGCCCCCCCCCCCCGGGTCCGGTAGAGGAGGTGCCGGCCCTGCTGGAGG 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MetAspProAlaAlaGlySerSerMetGluProSerAlaAspTrpLeuAl 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34 laValalaLeuProAsnAlaProAsnSerTyrGlyArgArgProIleGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  251 ACGCTGCCCGGGAGGCTTCCTGGACACGCTGGTGGTGCTGCTGCACCGGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  yAlaGluProAsnCysAlaAspProAlaThrLeuThrArgProValHisA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGGGCGCGCTGGACGTGCCTGGGGGCCGTCTGCCCGTGGACCT
                                                                                                                                                                                                                                                                                                            Gaps: 0
Percent Identity: 98.718
                                                                                                                                                                                                                                                                                          Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                               to: 471
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ID V53819 standard; cDNA; 471 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              151 ProSerAspileProAsp 156
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                                                                                                                                                                                                                                                                                     Quality: 789.00
Ratio: 5.090
Percent Similarity: 99.359
                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to: V11238
                                                                                                                                                                                                                                                                                                                                                                           alignment_block:
US-09-016-869A-2 x V11238
                                                                                                                                                                                                                                                                   alignment_scores:
Quality:
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51

67

20

20

67

84

Ношо

HOKE BASE

351

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Human mutant multiple tumour suppressor gene sequences - for production of recombinant mutant polypeptide(s) Claim 1; Columns 87-90; 72pp; English.
The present sequence the human multiple tumour suppressor gene 1 (MTS1), useful in cancer diagnosis.
Sequence 947 BP; 207 A; 271 C; 274 G; 195 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-SEP-1997 (first entry)

Human multiple tumour suppressor gene 1.

Human; multiple; tumour; suppressor; MTS1; cancer; diagnosis; ds.

Homo saplens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                134 laGlyGlyThrArgGlySerAsnHisAlaArgIleAspAlaAlaGluGly 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   450
                                  101 CGGGGGCGCTGCCCAACGCACCGAATAGTTACGGTCGGAGGCCGATCCAG 150
                                                                                                                  84 spalaalaargGluGlyPheLeuAspThrLeuValValLeuHisArgAla 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      117 uAlaGluGluLeuGlyHisArgAspValAlaArgTyrLeuArgAlaAlaA 134
                                                                                                                                                                                                            84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67 yAlaGluProAsnCysAlaAspProAlaThrLeuThrArgProValHisA
                                                                                      51 ValMetMetGlySerAlaArgValAlaGluLeuLeuLeuHisGl
Length: 156
Gaps: 0
Percent Identity: 98.718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Skolnick MH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       r72311 standard; cDNA; 947 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cannon-Albright LA, Kamb A,
WPI, 97-258217/23.
P-PSDB; W19251.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MYRI-) MYRIAD GENETICS INC. (UTAH ) UNIV UTAH RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           151 ProSerAspileProAsp 156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_name: N_Geneseq_36:T72311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-MAR-1994; US-215086.
18-MAR-1994; US-215087.
14-APR-1994; US-227369.
01-JUN-1994; US-251938.
17-MAR-1995; WO-U03537.
07-JUN-1995; US-474177.
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/*tag=
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Ratio: 5.090
nilarity: 99.359
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US-09-016-869A-2 x T72311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-MAR-1994;
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The present sequence encodes a human multiple tumour suppressor I (MTSI) protein. The sequence is homologous to the corresponding murine gene. Primers designed from the gene can be used to design primers to detect abnormalities i.e. polymorphisms which may predispose towards malignancies such as melanoma, leukaemia, astrocytoma, lymphoma, glioma, as well as tumours of e.g. the breast, thyroid, pancreas, uterus and kidneys.

Fig. 186 G; 64 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mouse multiple tumour suppressor gene segment - useful for primer
                                                                                                                                                                      301 GGGCGCGCGCTGGACGTGCGCGATGCCTGGGGCCGTCTGCCCGTGGACCT 350
                                                       ualaGluGluLeuGlyHisArgAspValAlaArgTyrLeuArgAlaAlaA 134
                                                                                                               351 Gecreaggaerregeccarceceargreecacegracereceeeerg 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA encoding a human multiple tumour suppressor 1 (MTS1) Human; multiple tumour suppressor 1 gene; MTS1; cancer; ds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MetAspProAlaAlaGlySerSerMetGluProSerAlaAspTrpLeuAl 17
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Gaps: 0
Percent Identity: 98.718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 from: 1 to: 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= a
150..151
/*tag= b
/note= "splice site"
478..458
/*tag= 'splice site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                _documentation_block:
V70583 standard; cDNA; 471 BP.
V70583;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-DEC-1998.
28-JUL-1995; 058735.
28-JUL-1995; US-508735.
07-JUN-1995; US-487033.
(MYRI-) MYRRAD GENETICS INC
JIANG P, Kamb A, Stone S;
WPI: 99-044585/04.
P-PSDB; W80524.
                                                                                                                                                                                                                                                                                                                           CCCTCAGACATCCCCGAT 468
                                                                                                                                                                                                                                                                                               ProSerAspileProAsp 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                 seq_name: N_Geneseq_36:V70583
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5.090
99.359
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*tag=
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US-09-016-869A-2 x V70583
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Percent Similarity:
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Homo sapiens

03-FEB-1999

451 151

misc_feature

misc_feature

alignment_scores

design

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alignment_scores:
                                                                                                                                                                                                             alignment_block
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                                                                                                                             Sednence
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WTS1; multiple tumour suppressor; diagnosis; cancer; germ-line mutation;
familial melanoma locus; MLM; predisposition; ds.
                                                                                                                                                                                                                                                                                  51 CACGGCCCGGGCCCGGGGTCGGGTAGAGGAGGTGCGGCGCCGCTGCTGCAGG 100
                                                                                                                                                                            200
                                                                                                                                                                                                                                           100
                                                                                                                                                                                                                                                    251 ACGCTGCCCGGGAGGCTTCCTGGACACGCTGGTGGTGCTGCACCGGGCC 300
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                                                                                                                                                                                                                                                                                                                                                                     134 laGlyGlyThrArgGlySerAsnHisAlaArgIleAspAlaAlaGluGly 150
                                                                                                              34
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                                                                                                                                                       17 aThralaalaalaargGlyargValGluGluValArgAlaLeuLeuGluA
                                                                                                                                                                                                                                                                                                                            uAlaGluGluLeuGlyHisArgAspValAlaArgTyrLeuArgAlaAlaA
                                                                                                                                                                                                                                                                                                                                                401 CGGGGGCACCAGAGGCAGTAACCATGCCCGCATAGATGCCGCGGAAGGT
                             1 MetAspProAlaAlaGlySerSerMetGluProSerAlaAspTrpLeuAl
                                                                                                                                                                                                                                           spAlaAlaArgGluGlyPheLeuAspThrLeuValValLeuHisArgAla
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/note= "splice site acceptor"
458
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         947
           <u>ب</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
         from: 1
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/note= "splice
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ID V11270 standard; cDNA; 947 BP.
AC V11270;
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                                                                                                                                                                                                                                                                                                                                                                                                             151 ProSerAspIleProAsp 156
                                                                                                                                                                                                                                                                                                                                                                                                                                   451 CCCTCAGACATCCCCGAT 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUL-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_name: N_Geneseq_36:V11270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US5739027-A.
14-APR-1998.
07-JUN-1995, 487033.
07-JUN-1995; US-214582.
18-MAR-1994; US-214582.
18-MAR-1994; US-215086.
18-MAR-1994; US-215087.
14-APR-1994; US-227369.
01-JUN-1994; WS-227369.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human MTS1 cDNA variant
        to: T72311
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WPI; 98-250421/22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        misc_feature
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         Align seg 1/1
                                                                                                                                                                                                                                                                                                                           117
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DNA specific for Multiple Tumour Suppressor IEI-beta gene - are useful for the diagnosis of cancers related to MTSIE1-beta multation(s) and their treatment
Disclosure; Column 89-90; 72pp; English.
This CDNA sequence encodes a variant of the human multiple tumour suppression protein, MTSI. The MTS gene locus is also referred to as the familial melanoma (MLM) gene locus, located on human chromosome 9p21.
Germ line mutations in MTS genes can be used in the diagnosis of predisposition to cancers, e.g. melanoma, leukaemia, astrocytoma, gliboblastoma, lymphoma, glioma, Hodgkin's lymphoma, CLL, and cancers of the pancreas, breast, thyroid, ovary, uterus, testis, kidney, stomach and rectum.
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Coding sequence 3 of the multiple tumour suppressor 1.
Multiple tumour suppressor 1; MTS-1; human; cancer; hybridisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          uAlaGluGluLeuGlyHisArgAspValAlaArgTyrLeuArgAlaAlaA 134
                                                                                                                                                                                                                                                            195 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67 yAlaGluProAsnCysAlaAspProAlaThrLeuThrArgProValHisA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84 spalaalaargGluGlyPheLeuAspThrLeuValValLeuHisArgAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           101 GlyAlaArgLeuAspValArgAspAlaTrpGlyArgLeuProValAspLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   351 GGCTGAGGAGCTGGGCCATCGCGATGTCGCACGGTACCTGCGCGCGGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51 ValMetMetMetGlySerAlaArgValAlaGluLeuLeuLeuHisGl
                                                                                                                                                                                                                                                                                                                                          Length: 156
Gaps: 0
Percent Identity: 98.718
                                                                                                                                                                                                                                                          274 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to: 947
                                                                                                                                                                                                                                                            271 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            from: 1
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                                                                                                                                                                                                                                                          207 A;
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ID V53851 standard; cDNA; 947
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5.090
99.359
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                                                                                                                                                                                                                                                            947 BP;
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Ratio:
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Claim 1; Fig 17, 73pp; English.

Claim 1; Fig 17, 73pp; English.

Claim 1; Fig 17, 73pp; English.

This is the nucleic Agequence of the invention. The MTS gene used in the method of the invention. The MTS gene is useful in the diagnosis and prognosis of human cancer, e.g. by standard nucleic hybridisation techniques, of patient samples. The standard nucleic hybridisation techniques, of patient samples. The vertors can be used for gene therapy is strategies to replace function of mutated protein in patients. Thase can also be used to construct protein mimetics, also for therapeutic strategies. In addition the expression constructs can also be used for recombinant production of MTS. Recombinant MTS can be used to screen for drugs to be used for cancer therapy, and the protein cancer for drugs to be used for cancer therapy, and the protein a call.

Sequence 947 BP; 207 A; 271 C; 274 G; 195 T;
                                                                                                                                                                                                                                                    Nucleic acids based on multiple tumour suppressor, MTS, sequences useful as hybridisation probes, primers and recombinant production of MTS in the diagnosis and treatment of cancers related to MTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34 laValAlaLeuProAsnAlaProAsnSerTyrGlyArgArgProIleGln 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              from: 1 to: 947
дs
mutation; gene therapy;
                                                           07-JUN-1995; 480810.

07-JUN-1995; US-480810.

07-JUN-1995; US-214581.

18-MAR-1994; US-215086.

18-MAR-1994; US-215086.

14-APR-1994; US-215087.

14-APR-1994; US-221369.

17-MAR-1995; WO-U03316.

(MYRI-) MYRIAD GENETICS INC.
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5.090
99.359
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US-09-016-869A-2 x V53851
                                                                                                                                                                                                                                     WPI; 98-494842/42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
               Homo sapiens.
US5801236-A.
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somatic
                                                                                                                                                                                                                    Kamb A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21
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The present sequence represents the cDNA sequence for a human multiple tumour suppressor 1 (MTS1) gene, including noncoding portions. The gene can be used to design primers to detect abnormalities 1.e. polymorphisms which may predispose towards malignancies such as melanoma, leukaemia, astrocytoma, lymphoma, glioma, as well as tumours of e.g. the breast, thyroid, pancreas, uterus and kidneys.

Sequence 947 BP; 207 A; 271 C; 274 G; 195 T;
                                                                                                                                                                                                                                                                                                                                                                                   cDNA encoding a human multiple tumour suppressor 1 (MTS1) protein. Human; multiple tumour suppressor 1 gene; MTS1; cancer; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse multiple tumour suppressor gene segment – useful for primer
134 laGlyGlyThrArgGlySerAsnHisAlaArgIleAspAlaAlaGluGly 150
                                                                                                           20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51 ValMetMetMetGlySerAlaArgValAlaGluLeuLeuLeuLeuHisGl
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Gaps: 0
Percent Identity: 98.718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag= b
/note= "splice site acceptor"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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/note= "splice s
458
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01-DEC-1998.
28-JUL-1995; 058735.
28-JUL-1995; US-508735.
07-JUN-1995; US-487033.
(MXRI-) MYRAD GENETICS INC.
Jang P, Kamb A, Stone S;
WPI; 99-044585/04.
                                                                                                                                                                                                                                                                                              seq_documentation_block:
ID V70615 standard; cDNA; 947 BP.
AC V70615;
                                                                                                                                                                                               451 CCCTCAGACATCCCCGAT 468
                                                                                                                                                                       151 ProSerAspileProAsp 156
                                                                                                                                                                                                                                                                                                                                                             03-FEB-1999 (first entry)
                                                                                                                                                                                                                                                        seq_name: N_Geneseq_36:V70615
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Ratio: 5.090
nilarity: 99.359
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US-09-016-869A-2 x V70615
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_scores:
                                         351
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Ratio:
Percent Similarity:
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PR 17-JUL-1995; U11787.

PR 17-JUL-1995; U11787.

PR 17-JUL-1995; U2-502881.

PR 17-JUL-1995; U3-502881.

PR 17-JUL-1995; U3-502881.

PR 17-JUL-1995; U3-502881.

PR 17-JUL-1995; U3-502881.

PR 27-132336/12.

PR WPI; 97-132336/12.

PR WPI; 97-132336/12.

PR PFEBB; W10627.

PR TEXECOSULE; F19 1a; 92pp; English.

PR CALLOLAR Sequence represents the codding sequence for the tumour suppressor.

PR CALLOLAR Sequence is joined to a promoter functional in eukaryotic cells.

PR CALLOLAR Sequence is joined to a promoter functional in eukaryotic cells.

PR CALLOLAR Sequence or interaction is involved in the control of cyclin-dependent.

A Inhabitory subunit, which is involved in the control of cyclin-dependent.

CALLOLAR SEQUENCE OF the encoded protein, cancer cells can be detected. When the nucleic acid molecule is in the sense orientation, the expression construct can be used to restore p16 function in a cell, particularly by construct can be used to restore p16 function in a cell, particularly by construct the molecule is in the sense orientation, the concern or melanoma. It may also have anti-angiogenic activity.

CALLOLAR SEQUENCE OF THISTORY OF THE MAD THE CONTROLAR SECONDARY OF THE SECONDAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            _documentation_block:
T60951 standard; DNA; 987 BP.
T60951;
28-007-1997 (first entry)
Tumour suppressor p16 coding sequence.
Tumour suppressor; p16; inhibitor; cyclin-dependent kinase 4; CDK4; cancer cell; lung cancer; bladder cancer; melanoma; restenosis; therapy; anti-angiogenic activity; hyperproliferative disorder; ss.
                  CGGGGGGCACCAGAGGCAGTAACCATGCCCGCATAGATGCCGGGAAGGT 450
                                                                                                                                                                                                                                                                                                                                                                                                                             134 laGlyGlyThrArgGlySerAsnHisAlaArgIleAspAlaAlaGluGly 150
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                                                                                                                                                                                                                                                                                                                           uAlaGluGluLeuGlyHisArgAspValAlaArgTyrLeuArgAlaAlaA 134
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                                                                                                                         spAlaAlaArgGluGlyPheLeuAspThrLeuValValLeuHisArgAla
                                                                                                                                                                                                                     251 ACGCTGCCCGGGAGGCCTTCCTGGACACGCTGGTGGTGCTGCACCGGGCC
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41. 511
/*tag= a /product Tumour suppressor pl6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     219 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         451 CCCTCAGACATCCCCGAT 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 151 ProSerAspileProAsp 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name: N_Geneseq_36:T60951
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1mmunoassay
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                                                                                                                                                                                                                                                                                                                                                                           351
                                                                                                                      84
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Length:

Quality: 789.00

alignment_scores:

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25-MAY-1999 (first entry)
Truncated p27/p16 fusion protein encoding DNA.
Truncated p27/p16 fusion protein encoding DNA.
Cyclin-dependent kinase; CDK, CDK/cyclin complex; inhibitory; restenosis; CDK-binding motif; endothelialisation; fusion protein; therapeutic; acne; intracellular; transcellular; transcytosis; vascular wound; repair; hair; smooth muscle; cardiovascular; arteriosclerotic; fibroriac disorder; cellular proliferation; rheumatcoid arthritis; diabetes; cirrhosis; graft; tumour; inflammation; neurodegeneration; periodontal; spermatogenesis; transcytostala; human; p27; p16; truncated; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fusion and chimaeric proteins including cyclin-dependent kinase binding motif – used for regulation of cell proliferation and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             390
                                                                                                                                                                                                                                      91 CACGGCCGCGCCCGGGGTCGGGTAGAGGAGGTGCGGGCGCGCTGCTGGAGG 140
                                                                                                                                                                                                                                                                                                       141 CGGGGGCGCTGCCCAACGCACCGAATAGTTACGGTCGGAGGCCGATCCAG 190
                                                                                                                                                                                                                                                                                                                                                                        191 GTCATGATGATGGGCAGCGCCCGAGTGGCGGAGCTGCTGCTGCTCCACGG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             spalaalaargGluGlyPheLeuAspThrLeuValValLeuHisArgAla 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GlyalaArgLeuAspValArgAspAlaTrpGlyArgLeuProValAspLe 117
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                                                                                                                                                                                                                                                                                                                                                                                                          84
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                                                                                                                                  aThralaalaalaargGlyargValGluGluValArgAlaLeuLeuGluA
                                                                                                                                                                                                                                                                      34 laValAlaLeuProAsnAlaProAsnSerTyrGlyArgArgProIleGln
                                                                                                                                                                                                                                                                                                                                       51 ValMetMetMetGlySerAlaArgValAlaGluLeuLeuLeuLeuHisGl
                                                                                                                                                                                                                                                                                                                                                                                                          yAlaGluProAsnCysAlaAspProAlaThrLeuThrArgProValHisA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGGGCGCGGGCTGGACGTGCCTGGGGCCGTCTGCCGTGGGGCCT
Gaps: 0
Percent Identity: 98.718
                                                                                                    ä
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29-JUL-1997; US-902572.
(MITO-) MITOTIX INC.
Beach DH, Gyutis J, Lamphere L;
WPI; 99-153770/13.
                                                                                                  from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   151 ProSerAspileProAsp 156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       X26233 standard; DNA; 737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name: N_Geneseq_36:X26233
5.090
                                                                                                to: T60951
                                                 alignment_block:
US-09-016-869A-2 x T60951
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P-PSDB; W95105
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                                                                                                  Align seg 1/1
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seq_name: N_Geneseq_36:X26234
                                              Claim 60; Page 84-85; 88pp; English.

Claim 60; Page 84-85; 88pp; English.

The invention relates to novel inhibitors of cyclin-dependent kinases

The invention relates to novel inhibitors of cyclin-dependent kinases

CDKs), particularly CDK/cyclin complexes. It provides a recombinant

transfection system (A) that comprises: (I) first gene construct

comprising a sequence encoding an inhibiting activity of a CDK,

linked to a transcription regulator functional in enkaryotic cells; (ii)

second gene construct comprising a sequence encoding a polypeptide that

promotes endothelialisation, and (iii) a gene delivery composition for

delivering the GCs to a cell for transfection. Also provided are nucleic

collinear process when FP enter the cell, and (ii) a therapeutic

collular process when FP enter the cell, and (ii) a transcellular

collular process when FP enter the cell, and (ii) a transcellular

consists of at least one CDK-binding moutlf and a TCP, See X26220 for

consists of the recombinant transfection system. The present
 for treatment of, e.g. vascular injury, cancers,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              112 ATGATGAGGCAGCGCCCGAGTGGCGGAGCTGCTGCTGCTCCACGGCGC 461
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AlaArgLeuAspValArgAspAlaTrpGlyArgLeuProValAspLeuAl 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCGCGGCTGGACGTGCCTGGGGGCCGTCTGCCCGTGGACCTGGC 611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 ASPProAlaAlaGlySerSerMetGluProSerAlaAspTrpLeuAlaTh 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ralaalaalaargGlyargValGluGluValArgAlaLeuLeuGluAlaV 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52 MetMetMetGlySerAlaArgValAlaGluLeuLeuLeuLeuHisGlyAl 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          aGluProAsnCysAlaAspProAlaThrLeuThrArgProValHisAspA 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGAGCCCAACTGCGCCCGCCCCCCCCCCCCGGCCCGTGCACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35 alAlaLeuProAsnAlaProAsnSerTyrGlyArgArgProlleGlnVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTGCCCGGGAGGGCTTCCTGGACACGCTGGTGGTGCTGCACCGGGCCGGG
                                                                                                                                                                                                                                                                                                                                                                                          Percent Identity: 99.355
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                                                                                                                                                                                                                                                                                                                                                                             Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to: 737
                                                                                                                                                                                                                                                                                                 227 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   from: 1
               fibrosis and neurodegeneration
                                                                                                                                                                                                                                                                                                    135 A;
                                                                                                                                                                                                                                                                                                                                                           788.00
5.117
99.355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to: X26233
                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_block:
US-09-016-869A-2 x X26233
                                                                                                                                                                                                                                                                                                    737 BP;
 differentiation,
                                                                                                                                                                                                                                                                                                                                            alignment_scores:
Quality:
                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                             Ratio:
                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                      protein.
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fibrosis and neurodegeneration

Staim 60, Page 85; 88pp; English.

Claim 60, Page 85; 88pp; English.

Comprising a sequence encoding an inhibitory polypeptide containing at comprising a sequence encoding an inhibiting activity of a CDK, linked to a transcription regulator functional in eukaryotic cells; (ii) casecond gene construct comprising a sequence encoding a polypeptide that promotes endothelialisation, and (iii) a gene delivery composition for delivering the GCs to a cell for transfection. Also provided are nucleic collivering the GCs to a cell for transfection. Also provided are nucleic collular process when FP enters the cell, and (ii) a transcellular collular process when FP enters the cell, and (ii) a transcellular collular process when FP enters the cell, and (ii) a transcellular consists of at least one CDK-binding motif and a TCP. See x26220 for consists of at least combinant transfection system. The present
                                                                                            25-MAY 1999 (first entry)
Truncated p27/p16 fusion protein encoding DNA.
Truncated p27/p16 fusion protein encoding DNA.
Cyclin-dependent kinase, CDK, CDK/cyclin complex; inhibitory; restenosis; CDK.binding motif; endothelialisation; fusion protein; therapeutic; acne; intracellular; transcellular; transcytosis; vascular wound; repair; hair; smooth muscle; cardiovascular; arteriosclerotic; fibrotic disorder; cellular proliferation; rheumatoid arthritis; diabetes; cirrhosis; graft; tumour; inflammation; neurodegeneration; periodontal; spermatogenesis; tachycardia; human; p27; p16; truncated; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fusion and chimaeric proteins including cyclin-dependent kinase binding motif - used for regulation of cell proliferation and differentiation, for treatment of, e.g. vascular injury, cancers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      456
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52 MetMetMetGlySerAlaArgValAlaGluLeuLeuLeuLeuHisGlyAl
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Gaps: 0
Percent Identity: 99.355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          295 G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             236 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Beach DH, Gyuris J, Lamphere L; WPI; 99-153770/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          137 A;
seq_documentation_block:
ID X26234 standard; DNA; 782 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5.117
99.355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-FEB-1999.
29-JUL-1998; U15759.
29-JUL-1997; US-902572.
(MITO-) MITOTIX INC.
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US-09-016-869A-2 x X26234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          782 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
WO9906540-A2.
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alignment_scores
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binding motif - used for regulation of cell proliferation and
differentiation, for treatment of, e.g. vascular injury, cancers,
fibrosis and neurodegeneration

Claim 60; Page 83; 88pp; English.

Claim 60; Page 83; 88pp; English.

Claim 60; Page 83; 88pp; English.

Clooks), particularly CDK/cyclin complexes. It provides a recombinant
transfection system (A) that comprises: (I) first gene construct
comprising a sequence encoding an inhibitory polypeptide containing at
comprising a sequence encoding an inhibitory polypeptide containing at
comprising a sequence encoding an inhibitory polypeptide that
comprising a sequence construct comprising a sequence encoding a polypeptide that
construct comprising a sequence encoding a polypeptide that
promotes endothelialisation, and (iii) a gene delivery composition for
collular process when FP enters the cell, and (ii) a therapeutic
collular process when FP enters the cell, and (ii) a transcellular
consists of at least one CDR-binding motif and a TCP. See x2620 for
consists of at least one CDR-binding motif and a TCP. See x2620 for
detailed uses of the recombinant transfection. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Truncated p27/pl6 fusion protein encoding DNA.

Truncated p27/pl6 fusion protein encoding DNA.

Truncated p27/pl6 fusion protein encoding DNA.

Cyclin-dependent kinase, CDK, CDK/cyclin complex; inhibitory; restenosis; CDK-binding motif; endothelialisation; fusion protein; therapeutic; acne; intracellular; transcettosis; vascular wound; repair; hair; smoth muscle; cardiovascular; arteriosclerotic; fibrotic disorder; cellular proliferation; rheumatoid arthritis; diabetes; cirrhosis; tumour; inflammation; neurodegeneration; periodontal; spermatogenesis; techygardia; human; p27; p16; truncated; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence represents a DNA encoding a human truncated p27/p16 fusion protein.
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                                      101
                                                                                                                                                                                                                                                                          aGluGluLeuGlyHisArgAspValAlaArgTyrLeuArgAlaAlaG 135
                                                                                                                                                                                                                                                                                                135 lyGlyThrArgGlySerAsnHisAlaArgIleAspAlaAlaGluGlyPro 151
                                                                                                                                                                                                                                                                                                                                                                                 102 AlaArgLeuAspValArgAspAlaTrpGlyArgLeuProValAspLeuAl 118
                                                                                                607 GCGCGGCTGGACGTGCGCGATGCCTGGGGCCGTCTGCCCGTGGACCTGGC
                 68 aGluProAsnCysAlaAspProAlaThrLeuThrArgProValHisAspA
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29-JUL-1998: U15759.
29-JUL-1997: US-902572.
(MITO-) MITOTIX INC.
Beach DH, Gyuris J, Lamphere L;
WPI: 99-153770/13.
P-PSDB; W95103.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_documentation_block:
ID X26231 standard; DNA; 1028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_name: N_Geneseq_36:X26231
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W09906540-A2.
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Truncated p27/p16 fusion protein encoding DNA.
Truncated p27/p16 fusion protein encoding DNA.
Truncated p27/p16 fusion protein encoding DNA.
Truncated p27/p16 fusion protein complex; inhibitory; restenosis; CVC:in-dependent kinase; DX; CDK-Cyclin complex; therapeutic; acnothmotif; endothelialisation; fusion protein; therapeutic; acnothmuscle; cardiovascular; transcytosis; vascular wound; repair; hair; smooth muscle; cardiovascular; arteriosclerotic; fibrotic disorder; cellular proliferation; relematoid arthritis; diabetes; cirrhosis; graft; tumour; inflammation; neurodegeneration; periodontal; spermatogenesis; tachycardia; human; p27; p16; truncated; ss.
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Length: 155
Gaps: 0
Percent Identity: 99.355
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29-JUL-1997; US-902572.
(MITO-) MITOTIX INC.
                                                        99.355
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US-09-016-869A-2 x X26231
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DX 22632 standard; DNA
AC 25-222 standard; DNA
AC 25-222
DE Truncated p27/p16 fur
Cyclin-dependent kink
CDK-binding mocif; en
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KW CDK-binding mocif; en
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KW cellular proliferation,
KW tumour; inflammation,
KW tumour; inflammation,
KW tachycardia; human; p
NO9906540-A2.
PD 11-FEB-1999.
PP 29-JUL-1999; US-9025;
PR 29-JUL-1999; US-9025;
PR 29-JUL-1999; US-9025;
PR ADTOTIX INC.
  Quality:
Ratio:
                                                     Percent Similarity:
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The invention relates to novel inhibitors of cyclin-dependent kinases are invention relates to novel inhibitors of cyclin-dependent kinases (CDKs), particularly CDK/cyclin complexes. It provides a recombinant transfection system (A) that complexes. It provides a recombinant comprising a sequence encoding an inhibitory polypeptide containing at least one CDK-binding motif for binding and inhibiting activity of a CDK, linked to a transcription regulator functional in eukaryotic cells; (ii) second gene construct comprising a sequence encoding a polypeptide that promotes endothelialisation, and (iii) a gene delivery composition for delivering the GCs to a cell for transfection. Also provided are nucleic cids encoding a fusion protein (FP) containing: (i) a therapeutic collular process when FP enters the cell, and (ii) a transcellular protein that alters a cellular process when FP enters the cell, and (ii) a transcellular consists of at least one CDK-binding motif and a TCP. See X26220 for detailed uses of the recombinant transfection system. The present consistence represents a DNA encoding a human truncated p27/p16 fusion
  binding motif - used for regulation of cell proliferation and differentiation, for treatment of, e.g. vascular injury, cancers, fibrosis and neurodegeneration
cell proliferation and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGGGCACCAGAGGCAGTAACCATGCCCGCATAGATGCCGCGGAAGGTCCC 1047
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99.355
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This sequence encodes a chimeric polypeptide of the invention. It was claims 13; Page 46-48; 58pp; English.

This sequence encodes a chimeric polypeptide of the invention. It was a this sequence encodes a chimeric polypeptides of the human p27 and p16 cDNA sequences. The chimeric polypeptides of the invention have cyclin-dependent kinase (CDK) binding motifis from at least two different proteins that bind to CDKS.

The protein controls proliferation and/or differentiation of cells, or particularly they inhibit cell-cycle progression. They can be used to creat a wide range of proliferative disorders, e.g. cancer, leukaemia, psoriasis, atherosclerosis, restenosis, chronic inflammation etc. They can also treat diseases associated with de-differentiation or consists and autonomous diseases of the peripheral degeneration of tissue, e.g. Alzhelmer's, Parkinson's or Huntington's diseases, gastric ulcers and autonomous diseases of the peripheral nervous system. Other applications include reducing growth of hair and protecting hair follicle cells against cytotoxic treatments, cosmetically to treat various forms of folliculitis, and to inhibit spermatogenesis or cogenesis. The chimeric proteins can also be used in vitro to maintain cells, especially neurons intended for testing specific activity of trophic factors, at selected points in the cell cycle. The proteins are more active inhibitors of the CDK/cyclin complex than binding motifs used the coll of th
                                                                                                                                        CDK inhibitory fusion protein p16p27 coding sequence.
Fusion gene; CDK inhibitor; cyclin-dependant kinase; p27 gene; p16 chimmeric polypeptide; human; binding motif; proliferation control; cell differentiation; cell-cycle inhibitor; proliferative disorder; tissue degeneration; therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chimeric inhibitor of cyclin dependent kinase - useful for gene therapy of cancer and other proliferative and differentiative
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Gaps: 0
Percent Identity: 99.355
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1. .1098
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                                                                    T74053 standard; cDNA; 1098
T74053;
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seq_name: N_Geneseq_36:T74053
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23-JAN-1996; US-589981.
(MITO-) MITOTIX INC.
Beach D, Gyuris J, Lan
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Sequence 1098
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CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/627,610
FILING DATE: 04-APR-1996
CLASSIFICATION: 800
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION UNDRER: 36,709
REPERENCE/DOCKET UNDRER: CSI-C
TELECOMMUNICATION INFORMATION:
TELEFONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                          & COCKFIELD
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US-09-016-869A-2 x US-08-627-610-1
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60 State Street
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Ratio: 5.128
Percent Similarity: 100.000
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STREET: 60 St
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
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US-08-627-610-1
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                                                                                                                                                                                                                         Particle Lan | Documentalition | Documentalition | Documentalition | Documentality | Section | Eard Orth | Sequence | Escotor | Lan | Buono | 1520.86 | 3.2e-77 | 10.26/ptodata/1/ina/5D_COMB.seq:05-08-316-511A-1 | 800.00 | 1520.86 | 3.2e-77 | 10.26/ptodata/1/ina/5D_COMB.seq:05-08-891-918A-1 | 800.00 | 1520.86 | 3.2e-77 | 10.26/ptodata/1/ina/5D_COMB.seq:05-08-891-918A-1 | 800.00 | 1520.86 | 3.2e-77 | 10.26/ptodata/1/ina/5D_COMB.seq:05-08-891-918A-1 | 800.00 | 150.08 | 3.2e-77 | 10.26/ptodata/1/ina/5D_COMB.seq:05-08-484-137-1 | 789.00 | 1507.24 | 1.8e-76 | 10.26/ptodata/1/ina/5D_COMB.seq:05-08-488-10-1 | 789.00 | 1507.24 | 1.8e-76 | 10.26/ptodata/1/ina/5D_COMB.seq:05-08-488-251-1 | 789.00 | 1507.24 | 1.8e-76 | 10.26/ptodata/1/ina/5D_COMB.seq:05-08-488-251-1 | 789.00 | 1507.24 | 1.8e-76 | 10.26/ptodata/1/ina/5D_COMB.seq:05-08-488-251-1 | 789.00 | 1507.24 | 1.8e-76 | 10.26/ptodata/1/ina/5D_COMB.seq:05-08-488-251-36 | 789.00 | 1507.21 | 4.5e-76 | 10.26/ptodata/1/ina/5D_COMB.seq:05-08-108-103-36 | 789.00 | 1500.21 | 4.5e-76 | 10.26/ptodata/1/ina/5D_COMB.seq:05-09-120-130-36 | 789.00 | 1500.21 | 4.5e-76 | 10.26/ptodata/1/ina/5D_COMB.seq:05-09-130-36 | 789.00 | 1500.21 | 4.5e-76 | 10.26/ptodata/1/ina/5D_COMB.seq:05-09-130-36 | 789.00 | 1307.88 | 2.3e-76 | 10.26/ptodata/1/ina/5D_COMB.seq:05-08-488-281-38 | 767.00 | 1457.91 | 1.0e-70 | 10.26/ptodata/1/ina/5D_COMB.seq:05-08-488-281-38 | 767.00 | 1447.84 | 1.0e-50 | 10.26/ptodata/1/ina/5D_COMB.seq:05-08-488-281-38 | 767.00 |
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OM of: US-09-016-869A-2 to: Issued_Patents_NA:*
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Database length: 68777915
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Query: US-09-016-869A-2
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GENERAL INFORMATION:
APPLICANT: Beach, David H.
APPLICANT: Serrano, Manuel
APPLICANT: Serrano, Manuel
APPLICANT: Delatho, Ronald A.
TITLE OF INVENTION: Transgenic Animals Having Modified Cell-Cycle
TITLE OF INVENTION: Regulation
NUMBER OF SEQUENCES: 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MetAspProAlaAlaGlySerSerMetGluProSerAlaAspTrpLeuAl 17
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us-09-016-869a-2.rni

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490
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Sequence 1, Application US/08893274

Fatent No. 5968821

GENERAL INFORMATION:

APPLICANT: Beach, David H.

APPLICANT: Berning Amount

APPLICANT: Berning Amount

APPLICANT: Hannon, Gregory J.

TILLE OF INVENTION: cell-Cycle Regulatory Proteins,

TITLE OF INVENTION: and Uses Related Thereto

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: FOLEY, HOAG & ELIOT LLP

STREET: One Post Office Square
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    441 CGGGGGCACCAGAGGCAGTAACCATGCCCGCATAGATGCCGCGGGAAGGT
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Gaps: 0
Percent Identity: 100.000
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US-09-016-869A-2 x US-08-306-511A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        151 ProSerAspileProAsp 156
                                                                                                                                 Percent Similarity: 100.000
                                                                                                              800.008
                                                                                                                Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Boston STATE: MA
; NAME/KEY:
; LOCATION:
US-08-306-511A-1
                                                                                           alignment_scores
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191 GTCATGATGAGGGCAGCGCCCGAGTGGCGGAGCTGCTGCTGCTCCACGG 240

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34 laValAlaLeuProAsnAlaProAsnSerTyrGlyArgArgProIleGln 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51 ValMetMetMetGlySerAlaArgValAlaGluLeuLeuLeuLeuHisGl 67
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALLDIe
OPPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/893,274
FILING DATE: 15-JULY-1997
CLASSIFICATION: 800
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US-09-016-869A-2 x US-08-893-274-1
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Percent Similarity: 100.000
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TOPOLOGY: linear
MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                 41..508
                                                                                                                                                                                                                                                                                                                                                                                                       ; NAME/KEY:
; LOCATION:
US-08-893-274-1
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seq_documentation_block:
    Sequence 1, Application US/08581918A
    Patent No. 6043030
    General Information:
    APPLICANT: Beach, David H.
    APPLICANT: Demetrick, Douglas J.
    APPLICANT: Demetrick, Douglas J.
    APPLICANT: Application Cell-Cycle Regulatory Proteins, and Uses:
    TITLE OF INVENTION: Related Thereto
    NUMBER OF SEQUENCES: 39
    CORRESPONDENCE ADDRESS: 30
    CORRESPONDEN
                                                                                                                                                                      uAlaGluGluLeuGlyH1sArgAspValAlaArgTyrLeuArgAlaAlaA 134
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CONDUTER: BARDABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC COMPALIDIE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARR: WordPed
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/581,918A
FILING DATE: 02-JAN 1996
FILING DATE: 30-JUN-1995
RIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/497,214
FILING DATE: 30-JUN-1995
FILING DATE: 30-JUN-1995
FILING DATE: 13-NOV-1994
FILING DATE: 14-SEP-1994
FILING DATE: 14-SEP-1994
FILING DATE: 15-MAY-1994
FILING DATE: 15-MAY-1994
FILING DATE: 15-MAY-1994
FILING DATE: 15-MAY-1994
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APPLICATION NUMBER: US 08/227,371
FILING DATE: 14-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/154,915
FILING DATE: 18-NOV-1993
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STREET: One Post Office Square
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        151 ProSerAspileProAsp 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         491 CCCTCAGACATCCCCGAT 508
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Æ
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84 spalaalaargGluGlyPheLeuAspThrLeuValValLeuHisArgAla 100
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PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/991,997
FILING DATE: 17-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36.709
REFERENCE/DOCKET NUMBER: MIV-071.06
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECAX: (617) 832-1299
TELEFAX: (617) 832-1299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_block:
US-09-016-869A-2 x US-08-581-918A-1
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Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          800.00
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MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                            41..508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: CDS
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US-08-581-918A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_scores
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Sequence 1, Application PC/TUS9504636

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: Related Thereto

NUMBER OF SEQUENCES: 10

COMPUTER READABLE FORM:

MEDIUM TYPE: 1DMPY disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII(text)

CURRENT APPLICATION NUMBER: PCT/US95/04636
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34 laValAlaLeuProAsnAlaProAsnSerTyrGlyArgArgProlleGln 50
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PRIOR APPLICATION UNBER:
APPLICATION NUMBER: US 08/346,147
FILING DATE: 29-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/306,511
FILING DATE: 14-SEP-1994
PRIOR APPLICATION NUMBER: US 08/248,812
FILING DATE: 25-NAY-1994
PRIOR APPLICATION NUMBER: US 08/248,812
FILING DATE: 14-PR-1994
FILING DATE: 14-APR-1994
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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US-09-016-869A-2 x PCT-US95-04636-1
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TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ratio: 5.128
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
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Ratio:
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PCT-US95-04636-1
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SEQUENCE CHARACTERISTICS

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PERMETAL INFORMATION:
APPLICANT: Skolnick, Mark H.
APPLICANT: Skolnick, Mark H.
APPLICANT: Cannon-Albright, Lisa A.
ADDRESSE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
CITY: Washington
STARE: DC
CONNTR: USA
COMPUTE: Expepy disk
COMPUTE: In-Apple 1995
SOFTWARE: Expepy disk
COMPUTE: USA
SOFTWARE: USA 08/215, 086
FILING DATE: 01-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USA 08/215, 086
FILING DATE: 10-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USA 08/215, 086
FILING DATE: 11-MAR-1994
PRIOR APPLICATION DATA:
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FILING DATE: 11-MAR-1994
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FILING DATE: 11-MAR-1994
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PRIOR APPLICATION DATA:
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FILING DATE: US-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USA 08/214, 582
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                                                                                                                                                                                                      341 GGGGCGCGCTGGACGTGCGCGATGCCTGGGGCCGTCTGCCCGTGGACCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REGISTRATION NUMBER: 24,884-109348-E
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_documentation_block:
    Sequence 1, Application US/08474177
    Patent No. 5624819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      151 ProSerAspileProAsp 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              491 CCCTCAGACATCCCCGAT 508
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84 spAlaAlaArgGluGlyPheLeuAspThrLeuValValLeuHisArgAla 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            401 CGGGGGCCACCAGAGGCAGTAACCATGCCCGCATAGATGCCGCGGAAGGT 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67 yAlaGluProAsnCysAlaAspProAlaThrLeuThrArgProValHisA 84
                                                                                                                                                                                                                                                                                                                                                                                                                      1 MetAspProAlaAlaGlySerSerMetGluProSerAlaAspTrpLeuAl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          251 ACGCTGCCCGGGAGGCTTCCTGGACACGCTGGTGGTGCTGCACCGGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51 ValMetMetGlySerAlaArgValAlaGluLeuLeuLeuHisGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_name: /cgn2_6/ptodata/1/ina/5B_COMB.seq:US-08-487-033-1
                                                                                                                                                                                                                                                                              Percent Identity: 98.718
                                                                                                                                                                                                                                                                                                                                                            to: 471
                                                                                                                                                                                                                                                 Length:
                                                                                                                                                                                                                                                                   Gaps:
                                                                                                                                                                                                                                                                                                                                                          from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_documentation_block:
; Sequence 1, Application US/08487033
; Patent No. 5739027
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                           alignment_block:
US-09-016-869A-2 x US-08-474-177-1
                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to: US-08-474-177-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Kamb, Alexander
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         151 ProserAspileProAsp 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        451 CCCTCAGACATCCCCGAT 468
                                                                                    ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
LENGTH: 471 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                               789.00
5.090
99.359
                                           TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                 Quality:
                                                                                                                                                                                                                                                                              Percent Similarity:
                                                                                                                                                                                                                                                                 Ratio:
                                                                                                                                                   ; NAME/KEY:
; LOCATION:
US-08-474-177-1
                                                                                                                                                                                                                                  alignment_scores
                                                                                                                                      FEATURE
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COUNTRY:

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151 ProSerAspileProAsp 156
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                                                                    ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP STREET: 1201 New York Avenue, Suite 1000 CITY: Washington STATE: DC
                                                                                                                                                                                                     COMPUTER LUSA

ZIP: JORO5

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk,
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURENT APPLICATION DATA:
APPLICATION WIMBER: US/08/487,033
FILING DATE: 07-JUN-1995
CLASSIFICATION: A35
PRICATION: A35
PRICATION: A35
PRILIANG DATE: 17-MR-1995
FILING DATE: 17-MR-1995
PRILIANG DATE: 17-MR-1995
PRILIANG DATE: 01-JUN-1994
FILING DATE: 01-JUN-1994
PRILIANG DATE: 18-MR-1994
PRILIANG DATE: 14-MR-1994
PRILIANG DATE: 18-MR-1994
PRILIANG DATE: 18-MR-1994
PRICK APPLICATION DATA: APR-1994
PRICK APPLICATION DATA: APR-1994
PRICK APPLICATION DATA: APR-1994
PRICK APPLICATION DATA: AMR-1994
PRICK APPLICATION NUMBER: US 08/214,582
PRICK AMPLICATION NUMBER: US 08/214,582
PRICK AMPLICATION NUMBER: US 08/214,582
PRICK AMPLICATION NUMBER: US 08/214,582
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Gaps: 0
Percent Identity: 98.718
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MTS1E1-Beta GENE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Inhen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24,
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_block:
US-09-016-869A-2 x US-08-487-033-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 471 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
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5.090
99.359
                      NUMBER OF SEQUENCES: 3/CORRESPONDENCE ADDRESS:
FITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1..471
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Ratio:
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: 11: MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; NAME/KEY:
; LOCATION:
US-08-487-033-1
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84 spAlaAlaArgGluGlyPheLeuAspThrLeuValValLeuHisArgAla 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          101 CGGGGGCGCTGCCCAACGCACCGAATAGTTACGGTCGGAGGCCGATCCAG 150
                                                                                                                                                                                                            151 GTCATGATGATGGGCAGCGCCCGAGTGGCGGAGCTGCTGCTGCTCCACGG 200
                                                                                                                                                                       67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 1201 New York Avenue, Suite 1000
CITY: Washington
                                                                                  34 laValAlaLeuProAsnAlaProAsnSerTyrGlyArgArgProIleGln
                                                                                                                                                                     51 ValMetMetMetGlySerAlaArgValAlaGluLeuLeuLeuLeuHisGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_name: /cgn2_6/ptodata/1/1na/5B_COMB.seq:US-08-480-810-1
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APPLICATION NUMBER: US/08/480,810
FILING DATE: 07-JUN-1995
CLASSIFICATION 1435
PRIOR APPLICATION DATE: PCT/US95/03316
FILING DATE: 17-MAR-1995
PRIOR APPLICATION NUMBER: PCT/US95/03316
FILING DATE: 01-JUN-1994
PRIOR APPLICATION NUMBER: US 08/251,938
FILING DATE: 01-JUN-1994
PRIOR APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US 08/215,086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_documentation_block:
    Sequence 1, Application US/08480810
    Patent No. S801236
    GENERAL INFORMATION:
    APPLICANT: Kamb, Alexander
    TITLE OF INVENTION: WTSL GENE
    NUMBER OF SEQUENCES: 36
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: Venable, Baetjer, HOW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIOM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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84 spalaalaargGluGlyPheLeuaspThrLeuValValLeuHisargala 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                251 ACGCTGCCCGGGAGGGCTTCCTGGACACGCTGGTGGTGCTGCACCGGGCC 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps: 0
Percent Identity: 98.718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            from: 1 to: 471
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,369
FILING DATE: 14-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-MAR-1994
ATTORNEY,AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
RECISTRATION NUMBER: 28 957
RECISTRATION NUMBER: 28 957
REFERENCE/DOCKET NUMBER: 24884-109348
TELECHONNICATION INFORMATION:
TELECHONE: 202-962-4810
INFORMATION FOR SEQ ID NO: 1:
CENGTH: 471 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to: US-08-480-810-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_block:
US-09-016-869A-2 x US-08-480-810-1
                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 789.00
5.090
99.359
                                                                                                                                                                                                                                                                                          MOLECULE TYPE: CDNA HYPOTHETICAL: NO ANTI-SENGT
                                                                                                                                                                                                                                                                                                                                                                                                         ; NAME/KEY: CDS
; LOCATION: 1..471
US-08-480-810-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality:
Ratio:
Percent Similarity:
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_scores:
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Sequence 1, Application US/08508735
Patent No. 5843756
GENERAL INFORMATION:
APPLICANT: Stone, Steven
APPLICANT: Alang, Ping
APPLICANT: Mamb, Alexander
TITLE OF INVENTION: MIS GENE AND THERAPEUTIC USE THEREOF
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESS:
ADDRESSEE: 1201 New York Avenue, Suite 1000
                                                                                                                                                              seq_name: /cgn2_6/ptodata/1/ina/5C_COMB.seq:US-08-508-735-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 20005
COMPUTER REDABLE FORM:
MEDIJUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/508,735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PPLICALL...
FILING DATE:
CLASSIFICATION: 435
RICASIFICATION DATA:
APPLICATION NUMBER: US to be assigned
FILING DATE: 07-JUN-1995
FILING DATE: 07-JUN-1995
PRIOR APPLICATION NUMBER: PCT/US95/0316
FILING DATE: 17-MR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REFERENCE/DOCKET NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 28,957
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAN: 202-962-4848
TELEFRAN: 202-962-8300
TELEFRAN: 202-962-8300
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; LOCATION: 457..458
; OTHER INFORMATION: /note= "Splice site"
US-08-508-735-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 471 base pairs TYPE: nucleic acid STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: 150..151
OTHER INFORMATION: /note-
                                                                           ORIGINAL SOURCE:
ORGANISM: Homo saplens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Washington
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                                                                                                                                                                                                      seq_documentation_block
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: lines
MOLECULE TYPE: CI
HYPOTHETICAL: NO
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE
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101 CGGGGGCGCTGCCCAACGCACCGAATAGTTACGGTCGGAGGCCGATCCAG 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length: 156
Gaps: 0
Percent Identity: 98.718
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/848,251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to: US-08-848-251-1 from: 1 to: 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REERENCE/DOCKET NUMBER: 24884-109348-G
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
                                                                                                                              CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
TIME DATE:
TIME DATE:
TIME DATE:
APPLICATION NUMBER:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
TIME DATE:
APPLICATION DATA:
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APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER:
TIME DATE:
TIME DATE:
APPLICATION DATA:
APPLICATION NUMBER:
BRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER:
BRIOR APPLICATION DATA:
APPLICATION NUMBER:
TIME DATE:
APPLICATION DATA:
APPLICATION NUMBER:
BRIOR APPLICATION DATA:
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APPLICATION NUMBER:
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US-09-016-869A-2 x US-08-848-251-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 471 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5.090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       789.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: CDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
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Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HYPOTHETICAL: NAMII-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORIGINAL SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; LOCATION:
US-08-848-251-1
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Sequence 1, Application US/08848251

Sequence 1, Application US/08848251

GENERAL INFORMATION:
APPLICANT: Skolnick, Mark H.
APPLICANT: Kamb, Alexander
APPLICANT: Cannon-Albright, Lisa A.
APPLICANT: Ramb, Alexander
APPLICANT: Machine METHOD FOR DETECTING PREDISPOSITION TO CANCER AT THE OF INVENTION: METHOD FOR DETECTING PREDISPOSITION TO CANCER AT THE OF INVENTION: GENE
TITLE OF INVENTION: GENE
TITLE OF INVENTION: GENE
STATES OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSES: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
CITY: Washington
STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               spAlaAlaArgGluGlyPheLeuAspThrLeuValValLeuHisArgAla 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           uAlaGluGluLeuGlyHisArgAspValAlaArgTyrLeuArgAlaAlaA 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17
                                                                                                                                                                                                                                                                                                             17 aThrAlaAlaAlaArgGlyArgValGluGluValArgAlaLeuLeuGluA 34
                                                                                                                                                                                                                                                                                1 MetAspProAlaAlaGlySerSerMetGluProSerAlaAspTrpLeuAl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_name: /cgn2_6/ptodata/1/1na/5D_COMB.seq:US-08-848-251-1
                                                                                   Percent Identity: 98.718
                                                                                                                                                                                                                          to: 471
                                                            Gaps:
                                                                                                                                                                                                                          from: 1
                                                                                                                                                                                                                       Align seg 1/1 to: US-08-508-735-1
                                                                                                                                      alignment_block:
US-09-016-869A-2 x US-08-508-735-1
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             151 ProSerAspileProAsp 156
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                         789.00
5.090
99.359
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                            Quality:
Ratio:
                                                                             Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20005
  alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 101
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24884-109348-B

REFERENCE/DOCKET NUMBER:

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GlyalaArgLeuAspValArgAspAlaTrpGlyArgLeuProValAspLe 117
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APPLICANT: Kamb, Alexander
TITLE OF INVENTION: MTS2 GENE
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
CITY: Washington
STREE: DC
COUNTRY: USA
ZIP: 20005
                                                                                                                                                                                                                                                                                                seg_name: /cgn2_6/ptodata/1/ina/5D_COMB.seg:US-08-486-047-1
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COMPUTER: IBM PC COMPATIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FPLICATION NUMBER: US/08/486,047
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                451 CCCTCAGACATCCCCGAT 468
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MEDIUM TYPE: Floppy
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134 laGlyGlyThrArgGlySerAsnHisAlaArgIleAspAlaAlaGluGly 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 101 cegegecerreceaacecaccaaragrracegreegecegarceae 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                201 CGCGGAGCCCAACTGCGCCGACCCCGCCACTCTCACCCGACCCGTGCACG 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                uAlaGluGluLeuGlyHisArgAspValAlaArgTyrLeuArgAlaAlaA 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             401 CGGGGGGCACCAGAGGCAGTAACCATGCCCGCATAGATGCCGCGGAAGGT 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34 laValAlaLeuProAsnAlaProAsnSerTyrGlyArgArgProlleGln 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67 yalaGluProAsnCysAlaAspProAlaThrLeuThrArgProValHisA 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MetAspProAlaAlaGlySerSerMetGluProSerAlaAspTrpLeuAl
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                                                                                                                                                                                                                                                                                                                                                                                  Percent Identity: 98.718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    from: 1 to: 471
                                                                                                                                                                                                                                                                                                                                                                      Gaps:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEPHONE: 202-962-4810
INFORMATION: 202-962-4810
SEQUENCE CHARACTERISTICS:
LENGTH: 471 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1 to: US-08-486-047-1
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US-09-016-869A-2 x US-08-486-047-1
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                                                                                                                                                                                                   ORIGINAL SOURCE:
ORGANISM: Homo saplens
                                                                                                                                                                                                                                                                                                                                                  789.00
5.090
99.359
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Ratio:
Percent Similarity:
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                                                                                                                                                                                                                                                                  ; LOCATION:
US-08-486-047-1
                                                                                                                                                                                                                                                    NAME/KEY:
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                                                                                                                                                                                                                                     FEATURE
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Align seg 1/1 to: US-09-120-130-1 from: 1

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seq_documentation_block:
    Sequence 1, Application US/09120130
    Patent No. 6037462
    GENERAL INFORMATION:
    APPLICANT: Kamb, Alexander
    TITLE OF INVENTION:
    NUMBER OF SEQUENCES: 36
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
    STREET: 1201 New York Avenue, Suite 1000
    CITY: Washington
    STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps: 0
Percent Identity: 98.718
                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURREMY APPLICATION DATA:
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us-09-016-869A-2 x us-09-120-130-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 471 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: HOMO sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               789.00
5.090
99.359
                                                                                                                                                        COUNTRY: USA ZIP: 20005
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: 11nea
MOLECULE TYPE: CI
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_scores:
Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: CDS
LOCATION: 1...
US-09-120-130-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
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101 CGGGGGCGCTGCCCAACGCACCGAATAGTTACGGTCGGAGGCCGATCCAG 150
                                                                                                                                                                                                                                                                             84 spalaalaargGluGlyPheLeuAspThrLeuValValLeuHisArgAla 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          101 GlyalaargLeuAspValArgAspAlaTrpGlyArgLeuProValAspLe 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    301 GGGGCGCGCGGGGCGCGCGATGCCTGGGGCCGTCTGCCCGTGGACCT 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           117 uAlaGluGluLeuGlyHisArgAspValAlaArgTyrLeuArgAlaAlaA 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50
                                                                                                                                                                      34 laValAlaLeuProAsnAlaProAsnSerTyrGlyArgArgProIleGln 50
                                                                                                                                                                                                                                                                                                                                        67 yAlaGluProAsnCysAlaAspProAlaThrLeuThrArgProValHisA 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP STREET: 1201 New York Avenue, Suite 1000 CITY: Washington STATE: DC
51 ValMetMetMetGlySerAlaArgValAlaGluLeuLeuLeuHisGl
                                                                                                                                                                                                                                                                                                                                                                201 GCGGGAGCCCAACTGCGCCGACCCCGCCACTCTCACCCGACCCGTGCACG
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FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION NUMBER:
FILING DATE: 07-UN-1995
APPLICATION NUMBER: PCT/US95/03316
APPLICATION NUMBER: 17-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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; Sequence 1, Application US/09115252
; Patent No. 6060301
; GENERAL INFORMATION:
; APPLICANT: Kamb, Alexander
; TITLE OF INVENTION: MTS1 GENE
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        451 CCTCAGACATCCCGGAT 468
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TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         101 CGGGGGCGCTGCCCAACGCAATAGTTACGGTCGGAGGCCGATCCAG 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           251 ACGCTGCCCGGGAGGCTTCCTGGACACGCTGGTGGTGCTGCACCGGGCC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 101 GlyAlaArgLeuAspValArgAspAlaTrpGlyArgLeuProValAspLe 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34 laValAlaLeuProAsnAlaProAsnSerTyrGlyArgArgProIleGln 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51 ValMetMetMetGlySerAlaArgValAlaGluLeuLeuLeuLeuHisGl 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17 aThrAlaAlaAlaArgGlyArgValGluGluValArgAlaLeuLeuGluA 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length: 156
Gaps: 0
Percent Identity: 98.718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               from: 1 to: 471
Align seg 1/1 to: US-09-115-252-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_block:
US-09-016-869A-2 x US-09-115-252-1
                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                    789.00
5.090
99.359
                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                      Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
                                                                                                                                                                                                                                                                                                          ANTI-SENSE: NO
ORIGINAL SOURCE
                                                                                                                                                                                                                                                                                                                                                     ; NAME/KEY:
; LOCATION:
US-09-115-252-1
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134 laGlyGlyThrArgGlySerAsnHisAlaArgIleAspAlaAlaGluGly 150
117 uAlaGluGluLeuGlyHisArgAspValAlaArgTyrLeuArgAlaAlaA 134
                                                                                                                                                                                                                                             351 GGCTGAGGAGCTGGGCCATCGCGATGTCGCACGGTACCTGCGCGCGGCTG 400
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Sequence 36, Application US/08474177
Sequence 36, Application US/08474177
Setent No. 564819
GENERAL INFORMATION:
APPLICANT: Skolnick, Mark H.
APPLICANT: Kamb, Alexander
APPLICANT: Kamb, Alexander
TITLE OF INVENTION: GERMLINE MUTATIONS IN THE MTS GENE
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: Venable, Baetjer, Howard & Civiletti, LLP 1201 New York Avenue, Suite 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name: /cgn2_6/ptodata/1/ina/5A_COMB.seq:US-08-474-177-36
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CIDITAR: USA

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IMP PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,177
FLING DATE: 07-JUN-1995
FRING APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/03537
FILING DATE: 17-MR-1995
FRING DATE: 01-JUN-1994
FILING DATE: 01-JUN-1994
FILING DATE: 18-MRR 1994
FRICH APPLICATION DATA:
APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-MRR 1994
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,086
FILING DATE: 18-MRR 1994
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,086
FILING DATE: 14-APR-1994
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/217,369
FILING DATE: 14-APR-1994
FRIOR APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-MRR-1994
FRIOR APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-MRR-1994
APPLICATION NUMBER: US 08/214,582
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 24
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
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                                                                                                                                                                                                                                                                                                                                                                                           451 CCCTCAGACATCCCCGAT 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 947 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Washington
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201 CGCGGGGCCCAACTGCGCCCGCCCCCCCTCTCACCCGACCCGTGCACG 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84 spAlaAlaArgGluGlyPheLeuAspThrLeuValValLeuHisArgAla 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    134 laGlyGlyThrArgGlySerAsnHisAlaArgIleAspAlaAlaGluGly 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51 CACGCCCCCCCCCCGCGTCGCGTAGAGGAGGTGCCGGCCCTGCTGGAGG 100
                                                                                                                                                                                                                                                                                                                                                                                             aThralaalaalaakgGlyArgValGluCluValArgAlaLeuLeuGluA 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ValMetMetGlySerAlaArgValAlaGluLeuLeuLeuLeuHisGl 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         yAlaGluProAsnCysAlaAspProAlaThrLeuThrArgProValHisA 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_name: /cgn2_6/ptodata/1/ina/5B_COMB.seq:US-08-487-033-36
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NAME/KEY: misc_feature
LOCATION: 151
OTHER INFORMATION: /note- "Splice site acceptor."
                                                                                                                                                                 LOCATION: 458
COTHER INFORMATION: /note= "Splice site acceptor.
US-08-474-177-36
                                                                                                                                                                                                                                                                                       Percent Identity: 98.718
                                                                                                                                                                                                                                                                                                                                                                 from: 1 to: 947
                                                                                                                                                                                                                                                                           Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 36, Application US/08487033
Patent No. 5739027
GENERAL INFORMATION:
APPLICANT: Kamb, Alexander
                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to: US-08-474-177-36
                                                                                                                                                                                                                                                                                                                     alignment_block:
US-09-016-869A-2 x US-08-474-177-36
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                        789.00
5.090
99.359
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                                                                                                                                                                                                                                           alignment_scores:
   Quality:
   Ratio:
   Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              251
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ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP STREET: 1201 New York Avenue, Suite 1000 CITY: Washington STATE: DC COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature

; LOCATION: 458

: OTHER INFORMATION: /note= "Splice site acceptor.

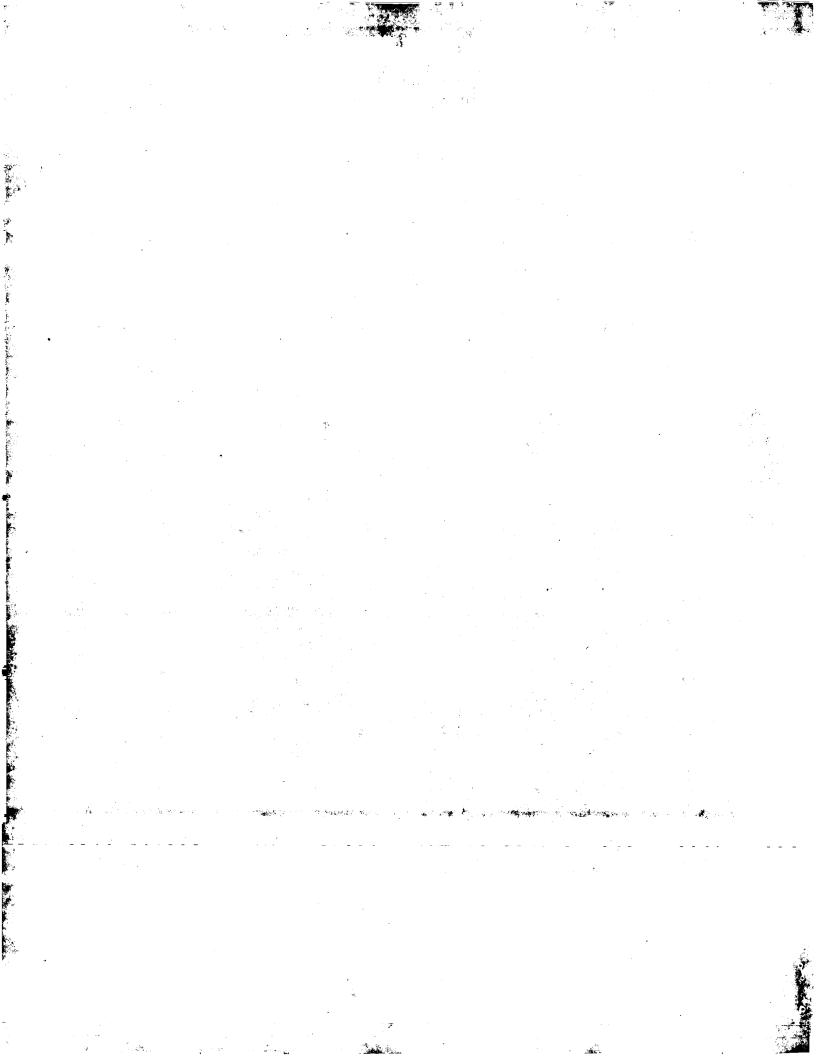
US-08-487-033-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: /note= "Splice site acceptor. FEATURE:
                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CNERNY APPLICATION NATM:
APPLICATION NUMBER: US/08/487,033
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps: 0
Percent Identity: 98.718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REERENCE/DOCKET NUMBER: 24884-109348-C
TELEPHONE: 202-962-4810
TELEPHONE: 202-962-4810
TELEPAX: 202-962-4830
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 947 Dase pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION 1435
PRIOR APPLICATION 1435
PRIOR APPLICATION 1435
PRIOR APPLICATION NUMBER: PCT/US95/03316
FILING DATE: 17-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,938
FILING DATE: 01-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-MAR-1994
PRIOR APPLICATION NUMBER: US 08/215,086
FILING DATE: 18-MAR-1994
PRIOR APPLICATION NUMBER: US 08/215,369
FILING DATE: 14-APR-1994
PRIOR APPLICATION NUMBER: US 08/217,369
FILING DATE: 14-APR-1994
PRIOR APPLICATION NUMBER: US 08/217,369
FILING DATE: 18-MAR-1994
APPLICATION NUMBER: US 08/217,569
FILING DATE: 18-MAR-1994
ATTORNEY APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-MAR-1994
ATTORNEY APPRICATION NUMBER: US 08/214,582
FILING DATE: 18-MAR-1994
ATTORNEY APPRICATION NUMBER: US 08/214,582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_block:
US-09-016-869A-2 x US-08-487-033-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  789.00
5.090
99.359
TITLE OF INVENTION: MTS
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
                                                                                                                                                                                                              20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION:
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to: 947 from: 1 Align seg 1/1 to: US-08-487-033-36

- 17 1 MetAspProAlaAlaGlySerSerMetGluProSerAlaAspTrpLeuAl
- 20

- yalaGluProAsnCysAlaAspProAlaThrLeuThrArgProValHisA 84 29
 - 201 GCGGGGCCCAACTGCGCCGACCCCGCCACTCTCACCCGACCCGTGCACG 250
- 101
 - 301 117
- 134 351
- 151

401



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NCI_CGAP
NCI_CGAP
SOBIES_t
NCI_CGAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

EX NCI-CGAP http://www.ncbi.nlm.nlh.gov/ncicgap.
NCI-CGAP http://www.ncbi.nlm.nlh.gov/ncicgap.
NCI-CGAP http://www.ncbi.nlm.nlh.gov/ncicgap.
NCI-CGAP http://www.ncbi.nlm.nlh.gov/ncicgap.

AL Unpublished (1997)

Tumor Gene Index

Contact: Robert Strausberg hh.D.

Tel: (301) 496-1550

Email: Robert Strausberg hh.D.

Tel: (301) 496-1550

Contact: Robert Strausberg hh.D.

CDNA Library Arrayed by: Renton. Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

Nww-bio.lln.jgov/bpry/mage/lnage/htmg

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was primed with a Not I: and Eco RI sites of the modified p773 vector:
Library is normalized, and was constructed by Bento
Library is normalized, and was constructed by Bento
Library is normalized, and was constructed by Bento
Library is normalized.
Library is n
                                                                                                                                                                                                             A1394605 566 bp mRNA EST 30-MAR-1999 tg13q05.x1 NCI_CGAP_CLIJ Homo sapiens cDNA clone IMAGE:2108696 3' similar to SW:CDN2_HUMAN P42771 CYCLIN-DEPENDENT KINASE 4 INHIBITOR A : contains LTR9.b3 TAR1 repetitive element ;, mRNA sequence.
  AA973236 or30910.sl N A1798040 wh80912.xl N AA625759 zu91907.sl S A1499733 tm91912.xl N
                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 517
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length: 113
Gaps: 0
Percent Identity: 98.230
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3.0e-18
9.6e-19
2.0e-17
  492.20
486.14
495.03
471.35
                                                                                                                                                                                                                                                                                                                                      AI394605.1 GI:4224152
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US-09-016-869A-2 x AI394605/rev
264.00
263.00
261.00
255.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98.230
                                                                                                                                   seq_name: gb_est20:AI394605
                                                                                                                                                                                       seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality:
Ratio:
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gb_est21:AI499733
                                                                                                                                                                                                                                                                                                                                                                                                     human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_scores:
                                                                                                                                                                                                                                                                                                                ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              source
                                                                                                                                                                                                                LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A1894605 tg13g05.x1 NCI_CGAP_CI
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A1633491 tt31g03.x1 NCI_CGAP_BI
A1633491 tt31g03.x1 NCI_CGAP_BI
A163418 x29395.x1 NCI_CGAP_BI
A257137 n174b05.s1 NCI_CGAP_BI
A4696118 w29305.x1 NCI_CGAP_BI
A4696116 HS_5075_A1_F12_T7 RPCI
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AQ496105 HS_5075_A1_F12_T7 RPCI
A1880671 WF15a09 XI SORTES_NFL
A1880671 WS15a09 XI SORTES_NFL
A1880671 WS15a08 XI SORTES_NFL
AN328497 GS02h12.71 NIH_MGC_4 H
AA98553 ZA44e11.71 NIT_MGC_4 H
AA085532 ZA44e11.71 NIT_MGG_4 H
AA08559 NIT5e01.X1 NIT_CGAP_UT
AA897759 NIT5e01.X1 NIT_CGAP_UT
AA897759 NIT5e01.X1 NIT_CGAP_UT
AA891759 NIT5E01.X1 NIT_CGAP_UT
AA899175 W5064.X1 NIT_CGAP_UT
AN591727 Ow5994.X1 SORTES_NSF
A1991727 Ow5994.X1 SORTES_NSF
A1818660 WK89511.X1 NIT_CGAP_UT
AA818660 WK89511.X1 NIT_CGAP_UT
A1818660 WK89511.X1 NIT_CGAP_UT
A334567 EST186468 COLON_CATCLUT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tb98f09.x1 NCI_CGAP_Cc
2175f06.s1 Stratagene
tm73d10.x1 NCI_CGAP_Br
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     wp78f11.x1 NCI_CGAP_Br
tm94b03.x1 NCI_CGAP_Br
UI-R-BT0-pu-g-12-0-UI.
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zm15a11.sl Stratagene
                                                                                                                                                                                                     -WODEL-frame+_p2n.model -DEV-x1p
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-ALIGN-15 -WODE-LOCAL -OUTPHT-pfs -NORM-ext -MINLEN-0
-LONGLOG -NO_XLPXY -WAIT -THREADS-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AI818660 w
AA314567 E
AI337358 t
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                                                                                                     About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
  out_format : pfs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11.9e-41

11.9e-41

11.8e-36

12.8e-36

13.6e-36

13.6e-35

13.6e-32

13.6e-27

13.6e-27

14.6e-32

15.6e-32

16.6e-36

17.6e-36

18.6e-36

19.6e-36

19.6e-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.7e-46
2.1e-46
4.9e-46
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611.62
596.06
594.71
583.90
563.18
564.27
551.21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Search information block:
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Query length: 156
Database: EST:*
Database sequences: 5247842
Database length: -2090053206
Search time (sec): 1223.270000
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                                                                                                                                                                            Command line parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence

9b_est26.AI394605

9b_est26.AI31381

9b_est26.AI870879

9b_est126.AI870879

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9b_est126.AI870879

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9b_est27.AAN910479

9b_est27.AAN910479

9b_est27.AAN910479

9b_est27.AAN910479

9b_est27.AAN910479957
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gb_est12:AA826886
gb_est1:AA069792
gb_est15:A1040505
gb_est17:A1149429
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gb_est21:AI500223
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                                                                                                                                                                                          Quality:
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                                                                                 BASE COUNT
ORIGIN
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TITLE
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COMMENT
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www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 845 Std Brror: 0.00
Seq primer: -400P from Gibco
High quality sequence stop: 444.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_documentation_block:
LOCUS AIR1381
LOCUS AIR1381
DEFINITION W.181431..x1 NOT_CGAP_BRD25 Homo sapiens CDNA clone IMAGE:2431317 3'
Similar to TR:Q16361 Q16361 CELL CYCLE NEGATIVE REGULATOR BETA FORM
// MRNA sequence.
ACCESSION A.1871381. G1:5545430
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1 (bases 1 to 590)
NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index On Oct 30, 1998 this sequence version replaced gi:3813427.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: Robert_Strausberg@nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone-"IMAGE:2431317"
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                                                                                                                                                                                                                                                                                                                                                         GGAGCTGCTGCTCCTCCACGGCGCGGAGCCCAACTGCGCNGACCCCGCCA 467
                                                                            77 hrLeuThrArgProValHisAspAlaAlaArgGluGlyPheLeuAspThr 93
aGluLeuLeuLeuHisGlyAlaGluProAsnCysAlaAspProAlaT 77
                   144 ArgileAspAlaAlaGluGlyProSerAspIleProAsp 156
                                                                                                                                                                                                                                                                                                                                                                                                                                            266 CGCATAGATGCCGCGGAAGGTCCCTCAGACATCCCCGGAT 228
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KEYWORDS
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adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized, and was constructed by Bento Soares and Mratia and Janado."
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 648)
NTH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
NTH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
On Apr 7, 1998 this sequence version replaced gi:3036295.
On Apr 7, 1998 this sequence version replaced gi:3036295.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: ATCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100 AlaGlyAlaArgLeuAspValArgAspAlaTrpGlyArgLeuProValAs 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          116 pLeualaGluGluLeuGlyHisArgAspValalaargTyrLeuargalaa 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    366 ccrggcrgaggagcrggccarcgcgargrcgcacggraccrgcgcggg 317
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Gaps: 0
Percent Identity: 100.000
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AW328496
AW328496.1 GI:6798992
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                                                                                                                                                                                                                                                                                                                                                                          US-09-016-869A-2 x AI871381/rev
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source

FEATURES

BASE COUNT

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                                                                                                                                                                                                                                                                                                                                                                                                                                             Bonaldo, Ph.D.
CDNA library Arrayed by: Greg Lennon, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
CDNA Sequencing by: Washington University Genome Sequencing Center
DNA Sequencing NGT-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llni.gov/bbrp/lmage/lmage.html
Insert Length: 819 std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 474.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                   Email: Robert_Strausbergenih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
Ph.D.
                   1 (bases 1 to 579)
NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BPGAP), Tumor Gene Index Unpublished (1998)
On May 18, 1998 this sequence version replaced gi:3136859.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                      cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
             dammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        505 ceececeaecceaacrececeaecceecaererereaecceaeccerec 456
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Gaps: 0
Percent Identity: 98.131
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seq_documentation_block:
LOCUS AI870879 579 bp mRNA EST 07-MAR-2000
DEFINITION W1701.x1 NOI_CGAP_BRN25 Homo sapiens cDNA clone IMAGE:2430933 3'
Similar to TR:Q16361 Q16361 CELL CYCLE NEGATIVE REGULATOR BETA FORM ', mRNA sequence.
ACCESSION AI870879 GI:5544847
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      109 CAGGTCATGATGATGGCCAGCGCCCGAGTGGCGGAGCTGCTGCTGCTCCA 158
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Gaps: 0
Percent Identity: 100.000
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US-09-016-869A-2 x AW328496
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_scores
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99

ORGANISM

VERSION KEYWORDS SOURCE

<u>:</u>

DEFINITION

150

ACCESSION

VERSION KEYWORDS

SOURCE

AUTHORS TITLE

JOURNAL

COMMENT

REFERENCE

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to reverse of: AI362049 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Robert_Strausberg@nih.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         256 GGTCCCTCAGACATCCCCGAT 236
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Align seg 1/1
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KEYWORDS
SOURCE
ORGANISM
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DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 884 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 321.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A1362049 580 bp mRNA EST 15-FEB-1999 qy39f07.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2014405 3' similar to TR:016361.016361 CELL CYCLE NEGATIVE REGULATOR BETA FORM A1362049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 580)

NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

Oritoria Cancer institute / National institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index

Conpolished (1998)

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert_Strausberg@nih.gov
                 cDNA Library Preparation: M. Bento Soares, Ph.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism-"Homo sapiens"
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/lab_host="DH108"
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                                                                                                    GlyProSerAspIleProAsp 156
                                                                                                                                             255 GGTCCCTCAGACATCCCCGAT 235
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5.067
98.131
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                                                                                                                                                                                                                                   seq_documentation_block:
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Ratio:
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source

FEATURES

alignment_block: US-09-016-869A-2 x Al362049/rev

BASE COUNT ORIGIN

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seq_documentation_block: 579 bp mRNA EST 02-DEC-1998
LOCUS AI198233 579 bp mRNA EST 02-DEC-1998
DEFINITION q155412.x1 NCI_CGAP_BRD25 Homo sapiens CDNA clone IMAGE:1860407 3'
Similar to TR:016361 016361 CELL CYCLE NEGATIVE REGULATOR BETA FORM ;contains LTR9.b3 TAR1 TAR1 repetitive element ;, mRNA sequence.
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DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
Gound through the I.M.A.G.E. Consortium/LINL at:
www-blo.llnl.gov/bbrpy/mage/hmage.html
Insert Length: 729 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 459.

1. 579
Location/Qualifiers
1. 579
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(Dases 1 to 579)

NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NAI/ONIAL Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAR), Tumor Gene Index
Unpublished (1998)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      307
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                                                                                                                                                                                                                                                                  pleualaGluGluLeuGlyHisArgAspValAlaArgTyrLeuArgAlaA 133
                                                                                                                                                                          506 ceccededecceaacrececeaerceeceaercrececeaaccerec 457
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                                                                                                                      83
   99
                                                                                                                   SGlyAlaGluProAsnCysAlaAspProAlaThrLeuThrArgProValH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GlnValMetMetMetGlySerAlaArgValAlaGluLeuLeuLeuHi
                                                         556 CAGGICAIGAIGAIGAGGCAGCGCICGAGIGGCGGAGCIGCIGCICCICCA
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alignment_scores:
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seg_documentation_block:
LOCUS AI765096 774 bp mRNA EST 21-DEC-1999
DEFINITION w148b08.x1 NCI_CGAP_CO16 Homo sapiens CDNA clone IMAGE:2393463 3'
similar to TR:Q13399 Q13399 HYPOTHETICAL 18.1 KDA PROTEIN ; contains
LTR9.b3 MER22 repetitive element ;, mRNA sequence.
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I (bases ttp://www.ncbi.nlm.nih.gov/ncicgap.
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tumor Gene Index
Unpublished (1997)
On Feb 22, 1999 this sequence version replaced g1:4283180.
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                            100 AlaGlyAlaArgLeuAspValArgAspAlaTrpGlyArgLeuProValAs 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCCGGGGCGCGGCTGGACGTGCCGCGATGCCTGGGGCCGTCTGCCCGTGGA 356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           66 sGlyAlaGluProAsnCysAlaAspProAlaThrLeuThrArgProValH 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83 isAspAlaAlaArgGluGlyPheLeuAspThrLeuValValLeuHisArg
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                                                                                                                                                                                                                                                      Gaps: 0
Percent Identity: 96.262
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AI765096.1 GI:5231605
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US-09-016-869A-2 x AI198233/rev
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5.009
99.065
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AUTHORS
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n can be
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Subtraction by Bento Soares and M. Fatima Bonaldo. " a 220 c 221 g 179 t 1 others
                                                                                               CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can l
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco
High quality sequence stop: 400.

Location/Qualifiers
                         lissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         115 laspLeualaGluGluLeuGlyHisArgAspValalaArgTyrLeuArgA 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99 ArgAlaGlyAlaArgLeuAspValArgAspAlaTrpGlyArgLeuProVa 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         493 IGCACGACGCIGCCCGGGAGGCCIICCIGGACACGCIGGIGGIGCIGCAC 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    443 GGGCCGGGGCGCGCTGGACGTGCGAATGCCTGGGGCCGTCTGCCCGT 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .....TGGGCAGCGCCCAGGGGCGCCCCCCCCTGTGGGCCATCGTG 644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 643 CTTATGCTATTGAGGAGCCCAGCGTTTAGGGCCAGCAGCGCTTCCTAGAA 594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49
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                                                  M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15 TrpLeuAlaThrAlaAlaAlaArgGlyArgValGluGluValArgAlaLe
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Gaps: 2
Percent Identity: 69.620
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Smail: Robert_Strausberg@nih.gov
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US-09-016-869A-2 x AI765096/rev
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4.336
77.215
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 708)

NOI/NIMDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index Unpublished (1998)

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert_Strausberg@nih.gov

Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A1363262 TO8 bp mRNA EST 16-FEB-1999 qy56f03.x1 NOI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2016029 3/ similar to TR:Q13195 Q13195 P16INK4/MTS1. [2] TR:Q13399 ; contains LTR9.b3 TAR1 repetitive element ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                           395 GAGAGCCCAGCGTCTAGGGCAGCAGCCGCTTCCTAGAAGACCAGGTCATG 546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   aArgGluGlyPheLeuAspThrLeuValValLeuHisArgAlaGlyAlaA 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       103 rgLeuAspValArgAspAlaTrpGlyArgLeuProValAspLeuAlaGlu 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGCTGGACGTGCGCGATGCCTGGGGCCGTCTGCCCGTGGACCTGGCTGAG 346
                                                                             2 AspProAlaAlaGlySerSerMetGluProSerAlaAspTrpLeuAlaTh 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18 rAlaAlaAlaArgGly.ArgValGluGluValArgAlaLeuLeuGluAla
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                                        Align seg 1/1 to reverse of: AI817709 from: 1
                                                                                                                 724 GACCTCCGNATTCGGCGCGCGTCGGNCCC
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  US-09-016-869A-2 x AI817709/rev
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LOCUS A1363262
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TITLE
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                  42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            495
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       445
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bonaldo, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                   seq_documentation_block:
LOCUS A1817709 DEFINITION WASSCIL.x1 NCT_CGAP_Brn25 Homo sapiens CDNA clone IMAGE:2413364 3'
DEFINITION WASSCIL.x1 NCT_CGAP_G13399 HYPOTHETICAL 18.1 KDA PROTEIN ;, MRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="anaplastic oligodendroglioma"
/lab_host="DH10B"
                                393 GGACCTGGCTGAGGAGCTGGGCCATCGCGATGTCGCCCGGTACCTGCCGC 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps: 4
Percent Identity: 67.251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    www.bio.llnj.gov/bbrp/image/image.html
Insert Length: 848 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 468.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="IMAGE:2413364"
/clone_11b="NCI_CGAP_Brn25"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                 149 GluGlyProSerAspileProAsp 156
                                                                                                                                   293 GAAGGICCCICAGACAICCCCGAI 270
                                                                                                                                                                                                                                                                                                                                  AI817709
AI817709.1 GI:5436788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   526.00
4.015
76.608
                                                                                                                                                                                            seq_name: gb_est25:AI817709
                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   - Ratio:
Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                             human.
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ORGANISM

ACCESSION VERSION KEYWORDS SOURCE REFERENCE AUTHORS

TITLE

JOURNAL

COMMENT

source

FEATURES

BASE COUNT

ORIGIN

136

source

FEATURES

BASE COUNT ORIGIN

440

390

```
SM Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 563)

S NCI-CARP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

L Onpublished (1997)

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert Strausberg@alh.gov

Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael

R. Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Vector: pr713D-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library NCI_CGAP_GC4 was prepared, and ss circles were made in vit.c sollowing HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made iform the same library (clonelDs 1257096-1258631, 1469064-1470983, and 1475592-1476743]. Subtraction by Bento Soares and M. Fatima Bonaldo. " a 158 c 169 g 124 t
                                                                                                                                                                                                                                                                                                                                                                                                                                         Bonaldo, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCT-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.libri.gov/Dbrp/lnage/Lnage.html

Insert Length: 613 Std Error: 0.00

Seq primer: -400P from Gibco

High quality sequence stop: 460.
wq34h12.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2473223 3'
similar to SW:CDN2_HUMAN P42771 CYCLIN-DEPENDENT KINASE 4 INHIBITOR
A ; , mRNA sequence.
A1994684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 uLeuLeuLeuHisGlyAlaGluProAsnCysAlaAspProAlaThrLeuT 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2413223"
/clone="lib="NCL_CGAP_GC6"
/tissue_type="pooled germ cell tumors"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to reverse of: A1954684 from: 1 to: 563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length: 111
Gaps: 0
Percent Identity: 94.595
                                                                                 AI954684.1 GI:5746994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-016-869A-2 x AI954684/rev
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4.849
95.495
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                                                                                                                               human.
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ORIGIN
    DEFINITION
                                                                                                                                              ORGANISM
                                                             ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                 AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                   JOURNAL
                                                                                                                                                                                                                REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURES
                                                                                                                                                                                                                                                                                                                       COMMENT
                                                                                                                                                                                                                             CONA Library Arrayed by: Greg Lennon, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:

www-blo.lin.gov/Dbrp/Anage/Amage.html

Insert Length: 872 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 394.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-MAR-2000
  Library Preparation: M. Bento Soares, Ph.D., M. Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100 AlaGlyAlaArgLeuAspValArgAspAlaTrpGlyArgLeuProValAs 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCCGGGGGGGCGCTGGGCGCGATGCCTGGGGCCGTCTGCCCGTGGA 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50 GlnValMetMetMetGlySerAlaArgValAlaGluLeuLeuLeuLeuHi 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66 sGlyAlaGluProAsnCysAlaAspProAlaThrLeuThrArgProValH 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83 isAspAlaAlaArgGluGlyPheLeuAspThrLeuValValLeuHisArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1 to reverse of: AI363262 from: 1 to: 708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps: 0
Percent Identity: 95.327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              240 GGTCCCTCAGACATCCCCGAT 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_block:
US-09-016-869A-2 x AI363262/rev
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5.019
97.196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_documentation_block:
LOCUS
A1954684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_scores:
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72

:: 2

129

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seq_documentation_block: 531 bp mRNA EST 14-DEC-1999
LOCUS A1633790 531 bp mRNA EST 14-DEC-1999
DEFINITION tt28e10.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2242122 3'
Similar to TR:016361 016361 CELL CYCLE NEGATIVE REGULATOR BETA FORM 'contains LTR9.b3 TAR1 repetitive element ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
1 (bases 1 to 531)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                              109 AlaTrpGlyArgLeuProValAspLeuAlaGluGluLeuGlyHisArgAs 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    125 pValAlaArgTyrLeuArgAlaAlaAlaGlyGlyThrArgGlySerAsnH 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  378 GCCIGGGGCCGICIGCCCGIGGACCIGGCIGAGGAGCIGGGCCAICGCGA 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      328 TGTCGCACGGTACCTGCGCGGGGGGGGGGGGCACCAGAGGCAGTAACC 279
                                                                                                                                                                                                                            59 ValAlaGluLeuLeuLeuLeuHisGlyAlaGluProAsnCysAlaAspPr
                                                                                                                                                                                                                                                       142 isAlaArgIleAspAlaAlaGluGlyProSerAspIleProAsp 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             278 AIGCCCGCAIAGAIGCCGCGGAAGTCCCTCAGACAICCCCGAI 235
Length: 98
Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                             Align seg 1/1 to reverse of: AI885362 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A1633790.1 GI:4685120
                                                                                                                              US-09-016-869A-2 x AI885362/rev
Quality: 510.00
Ratio: 5.204
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_name: gb_est23:A1633790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 human.
                                                                                                   alignment_block
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SOURCE
ORGANISM
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VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bonaldo, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: WI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

WWW-bio.llni.gov/Dbrp/Inage/image.html

Insert Length: 626 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 465.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_documentation_block:
LOCUS A1885362 528 bp mRNA EST 07-MAR-2000
DEFINITION *192104.x1 NCI_CGAP_Brn25 Homo sapiens CDNA clone IMAGE:2432407 3'
similar to SW:CDN2_HUMAN P42771 CYCLIN-DEPENDENT KINASE 4 INHIBITOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 528)

NCI/NTNDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NCI/NTNDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute / National Institute of Neurological Josecders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index Unpublished (1998)

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          M. Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="IMAGE:2432407"
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/lab_host="DH10B"
                       112 gLeuProValAspLeuAlaGluGluLeuGlyHisArgAspValAlaArgT 129
                                                                                                                                                                                                  yrLeuArgAlaAlaAlaGlyGlyThrArgGlySerAsnHisAlaArgIle 145
                                                                                                                                                                                                                          cDNA Library Preparation: M. Bento Soares, Ph.D.,
96 ValLeuHisArgAlaGlyAlaArgLeuAspValArgAspAlaTrpGlyAr
                                                                                                                           146 AspAlaAlaGluGlyProSerAspIleProAsp 156
                                                                                                                                                                                                                                                                                                                                                   264 GATGCCGCGGAAGGTCCCTCAGACATCCCCGAT 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AI885362.1 GI:5590526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: gb_est26:A1885362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            human.
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ORGANISM

REFERENCE

TITLE

JOURNAL

COMMENT

FEATURES

ACCESSION VERSION KEYWORDS SOURCE

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CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert_Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                      www-bio.linl.gov/bbrp/image/image.html
Insert Length: 623 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 454.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. .531 /
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2242122"
/clone_lib="NCI_CGAP_GC6"
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alignment_scores:

BASE COUNT

ORIGIN

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US-09-016-869A-2 x AI638416/rev
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5.122
98.990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_scores
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       108
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                                                                                                                                                                                                                                                          FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORIGIN
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NCI_CGAP_GC4 was prepared, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from a pool of 5,000 clones made
from the same library (cloneIDs 1257096-1258631,
1469064-1470983, and 145592-1476743). Subtraction by
Bento Soares and M. Fatima Bonaldo. "
10 thers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tt31g03.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2242420 3' similar to TR:Q16361 Q16361 CELL CYCLE NEGATIVE REGULATOR BETA FORM A1638416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCI-GAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI-GAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), National Cancer Institute, Cancer Genome Anatomy Project (CGAP), On Apr 7, 1988 this sequence version replaced gi:3036438.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Emmil: Robert_Strausberg@nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      108 AspAlaTrpGlyArgLeuProValAspLeuAlaGluGluLeuGlyHisAr 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gAspValAlaArgTyrLeuArgAlaAlaAlaGlyGlyThrArgGlySerA 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    331 CGATGICGCACGGIACCIGCGCGCGCGCGGGGGGGCACCAGAGGCAGIA 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              281 ACCATGCCGGATAGATGCCGGGGAAGGTCCCTCAGACATCCCCGAT 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    141 snHisAlaArgIleAspAlaAlaGluGlyProSerAspIleProAsp 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           euaspThrLeuValValLeuHisArgAlaGlyAlaArgLeuAspValArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to reverse of: AI633790 from: 1 to: 531
                                                                                                                                                                                                                                                                                                                                                                  Length: 99
Gaps: 0
Percent Identity: 98.990
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98.990
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LOCUS A1638416
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AUTHORS
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KEYWORDS
SOURCE
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2 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_documentation_block:
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DEFINITION wz93905.x1 NCI_CGAP_Brn25 Homo sapiens CDNA clone IMAGE:2566424 3'
similar to TR:Q16361 Q16361 CELL CYCLE NEGATIVE REGULATOR BETA FORM
                                                                                               Sequencing Center
information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDNA Library Preparation: M. Bento Soares, Ph.D., N. Bonaldo, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

CDNA Sequencing by: Washington University Genome Sec Clone distribution: NCI-CGAP clone distribution infound through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbpy/image/image.html
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Seg primer: -400P from Gibco
High quality sequence stop: 462.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AspalaTrpGlyArgLeuProValAspLeuAlaGluGluLeuGlyHisAr 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            378 GATGCCTGGGGCCGTCTGCCCGTGGACCTGGCTGAGGAGCTGGGCCATCG 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gAspValAlaArgTyrLeuArgAlaAlaAlaGlyGlyThrArgGlySerA 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               141 snHisAlaArgIleAspAlaAlaGluGlyProSerAspIleProAsp 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58 ArgvalAlaGluLeuLeuLeuLeuHisGlyAlaGluProAsnCysAlaAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length: 99
Gaps: 0
Percent Identity: 97.980
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ORGANISM

ACCESSION

VERSION KEYWORDS SOURCE

AUTHORS TITLE

REFERENCE

JOURNAL

COMMENT

FEATURES

```
AL Unpublished (1997)

On Jan 14, 1998 this sequence version replaced gi:1877968.

On Jan 14, 1998 this sequence version replaced gi:1877968.

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert Strausbergenih.gov.

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CLONG distribution: NOT-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LiNL at:

www-bio.llnl.gov/bbry/image/image.html

Insert Length: 755 Std Error: 0.00

Seq primer: -40ml3 fwd. ET from Amersham

High quality sequence stop: 1000 Amersham

High quality sequence stop: 1000 Amersham

High quality sequence stop: 1000 Amersham
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DEFINITION n174b05.s1 NCI_CGAP_Br2 Home sapiens cDNA clone IMAGE:1056569 3'
similar to SW:CDN2_HUMAN P42771 CYCLIN-DEPENDENT KINASE 4 INHIBITOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Vector: pT713D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from pooled bulk breast tumor tissue, and was then primed with a Not I oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT713 vector. This library is the normalized version of NCI_CGAP_BT1.1. Library was constructed by Bento Soares and M. Fatina Bonaldo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 599) NCI-GAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (GGAP),
                                                                                                                                                     133 laAlaGlyGlyThrArgGlySerAsnHisAlaArgIleAspAlaAlaGlu 149
                                                  preualaGluGluLeuGlyHisArgAspValAlaArgTyrLeuArgAlaA 133
                                                                                                                                                                                                        306 CIGCGGGGGCACCAGAGGCAGIAACCAIGCCCGCAIAGAIGCCGCGGAA 257
                                                                                106 GCCGGGGGGCGCGTGGGGGGGCCTGGGGGCCGTCTGCCGGGGA
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163 c 179 g 134 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
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                                                                                                                                                                                                                                                           GlyProSerAspileProAsp 156
                                                                                                                                                                                                                                                                                                              256 GGTCCCTCAGACATCCCCGAT 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA557137.1 GI:2327614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A ; mRNA sequence.
AA557137
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                                                                                                                                                                                                                                                                                                                                                           seq_name: gb_est9:AA557137
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AUTHORS
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KEYWORDS
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                                                  116
                                                                                                                                                                                                                                                           150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bonaldo, Ph.D. controlled by: Greg Lennon, Ph.D. controlled by: Greg Lennon, Ph.D. controlled by: Rashington University Genome Sequencing Center Clone distribution: NGI-CGAP clone distribution in Toward through the I.M.A.G.E. Consortium/LLNL at:

Www.bio.llnl.gov/bbrp/image/image.html
Seq primer: 40UP from Gibco
High quality sequence stop: 461.
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1 (bases 1 to 579)

NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NSIORIAGERS and Stroke, Brain Tumor Genome Anatomy Project (CGAP/PRIGAP), Tumor Gene Index

Unpublished (1998)

On Oct 6, 1998 this sequence version replaced gi:3705694.

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Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                            Email: Robert_Strausbergenih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100 AlaGlyAlaArgLeuAspValArgAspAlaTrpGlyArgLeuProValAs 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83 isAspAlaAlaArgGluGlyPheLeuAspThrLeuValValLeuHisArg 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50 GlnValMetMetGlySerAlaArgValAlaGluLeuLeuLeuLeuHi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to: 579
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Percent Identity: 95.327
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AW006218
AW006218.1 GI:5854996
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US-09-016-869A-2 x AW006218/rev
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4.654
97.196
                                                                                                     Homo sapiens
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Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 113
                                                                                human.
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119
484.00
Quality:
Ratio:
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Align seg 1/1

BASE COUNT

Run on:

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AR052786 Sequence
141160 Sequence
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157075 Human pl4-C
AF0000049 Homo sapi
875756 p15-cyclin
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141151 Sequence
141151 Sequence
141151 Sequence
AR062774 Sequence
141148 Sequence
141148 Sequence
141148 Sequence
141148 Sequence
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S75756
AC000049
S69805
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AR037497
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                                                                                                      1 GAGGACTCCGCGACGGTCCG......AGGCTGCCAACGGGGAGCGG 837
        GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                           Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                       - nucleic search, using sw model
                                                                                                                     IDENTITY_NUC Gapox 1.0
                                                                                    US-09-016-869A-3
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S78535 tumor suppr
U26727 Human pl6IN
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AR057505 Sequence
AR057785 Sequence
141159 Sequence
1359804 MTS1-multip
359802 Homo sapien
U12819 Human p16-I
AR001316 Sequence
AR05776 Sequence
AR052776 Sequence
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FGRRalQvwmgSarvaellllhgaepncadPatltrpvhdaaregfldtlvvlhrag
Arldvrdawgrlpvdlaeerghrdvagylrtatgd"
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 837)
Hannon,G.J. and Beach,D.
p15INK4B is a potential effector of TGF-beta induced cell cyc.
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/codon_start=1

/product="CDK inhibitory protein"

/protein_id="AAA50282.1"

/db_xref="G1:556198"
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; Pred. No. 3.2e-129;
0; Mismatches 0;
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/db_xref="taxon:9606"
/cell_line="Hacar"
/cell_type="keratinocyte"
/clone="pl5INK4B/HA5"
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CDK inhibitory protein.
Homo sapiens CDNA to mRNA.
Homo sapiens
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Best Local Similarity 100.
Matches 837; Conservative
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241 AGCAGCGTGGGAAAGAAGGGAAGAGTGTCGTTAAGTTTACGGCCAACGGTGGATTATATCCG 300
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                AAAGCCCGGAGCTAACGACCGGCCGCTCGGCACTGCACGGGGCCCCAAGCCGCAGAAA 180
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MTSIEL: beta. gene
Patent: US 5739027-A 15 14-APR-1998;
Location/Qualifiers
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AAAAGCCCGGAGCTAACGACCGGCCGCTCGG-CACTGCACGGGGCCCCAAGCCGCAGAAG
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Pred. No. 7.6e-103;
0; Mismatches 8;
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Sequence 15 from patent US 5843756.
AR062786.1 GI:5990477
Location/Qualifiers
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                /organism="unknown"
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Probes for MTS1 gene and polynucleotides encoding mutant MTS1 genes
Patent: US 5801236-A 15 01-SEP-1998;
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Pred. No. 7.6e-103;
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Sequence 15 from patent
AR037506
AR037506.1 GI:5955362
                Query Match
Best Local Similarity 97.9%;
Matches 730; Conservative
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Pred. No. 7.6e-103;
0; Mismatches 8;
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Stone, S., Jiang, P. and Kamb, A.
Mouse MTSI gene
Patent: US 5843756-A 15 01-DEC-1998;
Location/Qualifiers
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Pred. No. 7.6e-103;
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Skolnick,M.H., Cannon-Albright,L.A.
Germline mutations in the MTS gene
Patent: US 5624819-A 15_29-APR-1997;
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Best Local Similarity 97.9%;
Matches 730; Conservative
GI:2081750
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1. 738
/organism="Homo sapiens"
/db_xref="taxon:9606"
322. 738
/codon_start=1
/product="p14-DK inhibitor"
/product
                                                                                                                                                               Homo saplens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 738)
Guan, K.L., Jenkins, C.W., Li, Y., Nichols, M.A., Wu, X., O'Keefe, C.L.,
Matera, A.G. and Xiong, Y.
Growth suppression by pl8,
pl4INK4B/MTS2-related CDK6 inhibitor, correlates with wild-type pRb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Guan, Biological Chemistry,
Catherine, Ann Arbor, MI 48109,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAAGGGAAGAGTGTCGTTAAGTTTACGGCCAACGGTGGATTATCCGGGCCGCTGCGCGTC
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                          HSU17075 738 bp MRNA PRI Human p14-CDK inhibitor MRNA, complete cds. U17075
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Pred. No. 5.5e-102;
0; Mismatches 10;
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95095079
                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (09-NOV-1994) Kun-Liang
Iniversity of Michigan, 1301 East
USA
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Best Local Similarity 97.8%;
Matches 714; Conservative
                                                                                                     U17075.1 GI:639715
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                                                                                                                                                  human.
                                                         DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
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                                                                                                                                                                   ORGANISM
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AUTHORS
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MEDLINE
RESULT
HSU17075
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/nous- +...
/codon_start-1
/codon_start-1
/product-"alternative spliced form of p15 CDK inhibitor:
/protein_id="AAB69989.1"
/db_xref="G1:2257935"
/translation="MREBNKGMSAGGSDEGLASAAARGLVEKVROLLEAGADPNGVN
RFGRRAIQVAGAPGRRRQGARERRGARFRIGAGT"
RFGRRAIQVAGAPGRRRQGARERRGAGT
338 g 120 t
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Tsubari,M., Tilhonen,E. and Lalho,M.
Direct Submission
Submitted (20-MAY-1997) Department of Virology, Haartman Institute,
University of Helsinki, P.O. Box 21, Helsinki 00014, Finland
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases I to 859)
Tsubari,M., Tilhonen,E. and Laiho,M.
Cloning and characterization of p10, an alternatively spliced of p15 cyclin-dependent kinase inhibitor
                                                                                                                                                                                                                                                                                                                                                        731
                                                                                                                                                                                                                                                                                                                                                                             669 CGTGGACTTGGCCGAGGAGCGGGGCCACCGCGAGGTTGCAGGGTACCTGCGCACAGCCAC 728
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612 GGTGGTGCTGCACCGGGCCGGGCTGGACGTGCGCGGATGCCTGGGGTCGTCGCCTGCCC
                                                                                     GGGCAGCGCCGCGTGCTGCTGCTGCTCCACGGCGCGCGAGCCCAACTGCGCAGA
                                                                                                                                                                                                  GGTGGTGCTGCACCGGGCCGGGGCGGGCTGGACGTGCGCGATGCCTGGGGGTCGTCTGCC
                                                                                                                                                                                                                                                                                                                                                      CGTGGACTTGGCCGAGGGGGCCACCGCGACGTTGCAGGGTACCTGCGCACAGCCAC
                                                                                                                                                                             CCCTGCCACTCTCACCCGACCGGTGCATGATGCTGCCCGGGAGGGCTTCCTGGACACGCT
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    . 859
    /organism="Homo sapiens"
    /db_xref="taxon:9606"

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/note="p10"
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/protein_id="AbD14186.1"
/db_xref="GI:4261886"
/translation="MREENKGMPSGGGSDEGLASAAARGLVEKVRQLLEAGADPNGVN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              369 GGAGCAGCGTGGGAAAGAAGGGAAGAGTGTCGTTAAGTTTACGGCCAACGGTGGATTATC 428
Cancer Res. 54 (24), usus core to S5079408
GenBank staff at the National Library of Medicine created this entry [NOBI glbbsq 161516] from the original journal article.
Location/Qualifiers
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8
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Pred. No. 4.1e-60;
0; Mismatches 8; Indels 8;
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Homo sapiens Chromosome 9p21 Cosmid Clone c86,
AC000049
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                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
458. 613
/partial
/gene="pl5"
                                                                                                                                                                                                                                D-dependent
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protein/pl5 product 458. .613
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96.7%;
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1 215 c
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Best Local S
Matches 471
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 753)
Jen,J.; Harper,J.W., Bigner,S.H., Bigner,D.D., Papadopoulos,N., Markowitz,S., Willson,D.K., Kinzler,K.W. and Vogelstein,B.
Deletion of p16 and p15 genes in brain tumors
                                                                                                                                                                                                                                                                                                                                                          548
                 246
                                                                                                                                                                        314
                                                                                                                                                                                                   306
                                                                                                                                                                                                                              374
                                                                                                                                                                                                                                            GGGTCTGGCCA---CGCCGGGGGGCACTAGTGGAGAAGGTGCGACACTCCTGGGAAGC 431
                                                                                                                                                                                                                                                                                                              367 GGTCTGGCCAGCGCCGCGCGCGGGACTAGTGGAGAAGGTGCGACAGCTCCTGGAAGC 426
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/protein_id="AAD14049.1"
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/db_xref="GI:4261749"
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VVLHRGCARLDVRDAWGRLPVDLAEBERGHRDVAGYLRTATGD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note-"multiple tumor suppressor 2/cyclin-dependent kinase 4 inhibitor p16; This sequence comes from Fig. 2; Map location 9p21"
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   25247 GACAGCTCCTGGAAGCCGGCGCGGATCCCAACGGAGTCAACCGTTTCGGGAGGCGCGCGA 25306
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 457)
Kamb,A., Gruis,N.A., Weaver-Feldhaus,J., Liu,Q., Harshman,K.,
Tavtgian,S.V., Stockert,E., Day,R.S. 3rd, Johnson,B.E. and
Skolnick,M.H.
A cell cycle regulator potentially involved in genesis of many
tumor types
                                                                                                                                                              S69805 457 bp DNA PRI 23-SEP-1994 MTS2-multiple tumor suppressor 2/cyclin-dependent kinase 4 inhibitor pi6 (cosmid c5 region, exon 2) (human, melanoma cell line, Genomic Mutant, 457 nt].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 146819] from the original journal article. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98 CAGGICAIGAIGAIGGCCAGCGCCCGCGIGGCGGAGCIGCIGCIGCICCACGGCGCGCGGAG 157
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100.0%; Pred. No. 1.9e-50;
Live 0; Mismatches 0;
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/db_xref-"taxon:9606"
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/note="multiple tu
4 inhibitor pl6"
101. 361
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Submitted (18-Aug-1999) Department Of Chemistry And Biochemistry,
Submitted (18-Aug-1999) Department Of Chemistry And Biochemistry,
OK 73019, USA
ON Aug 5, 1999 this sequence version replaced gi:5649357.
Location/Qualifiers
1. .44160
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="9"
                                                                                                                                                                                                                                                                                                              Submitted (30-OCT-1996) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24890 GCGCTAGGCGCTTTTTCCCAGAAGCAATCCAGGCGCGCCGCTGGTTCTTGAGCGCCAGG 24949
                                                                                                                                                          Cosmid clone c86 derived from Homo saplens chromosome 9p21 and including coding sequence for p15/CDK-INK4b
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGGGCGGCAGCGATGAGGGTCTGGCCA---CGCCGGCGGGGACTAGTGGAGAAGGTGC 415
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Left Neighbor sequenced in this center: c66."
9089 c 8707 g 12511 t
                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 44160)
Sveen,L., Olopade,F.I. and Rowley,J.D.
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                                                                                                                                            Unpublished
2 (bases 1 to 44160)
Burlan, D.M., Mitchell, N.
Cosmid clone c86 derived
 GI:5705995
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4 (bases 1 to 44160)
Burlan, D. and Roe, B.A.
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Probes for MTS1 gene and polynucleotides encoding mutant MTS1 genes
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43.0%; Score 360; DB 5;
Best Local Similarity 100.0%; Pred. No. 1.4e-50;
Matches 360; Conservative 0; Mismatches 0;
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Kamb.A.

MTSIE1.beta. gene
Patent: US 5739027-A 5 14-APR-1998;
Location/Qualifiers
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Sequence 5 from patent US 5801236.
AR037497
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Sequence 5 from patent US 5739027
AR001317
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/organism="unknown"
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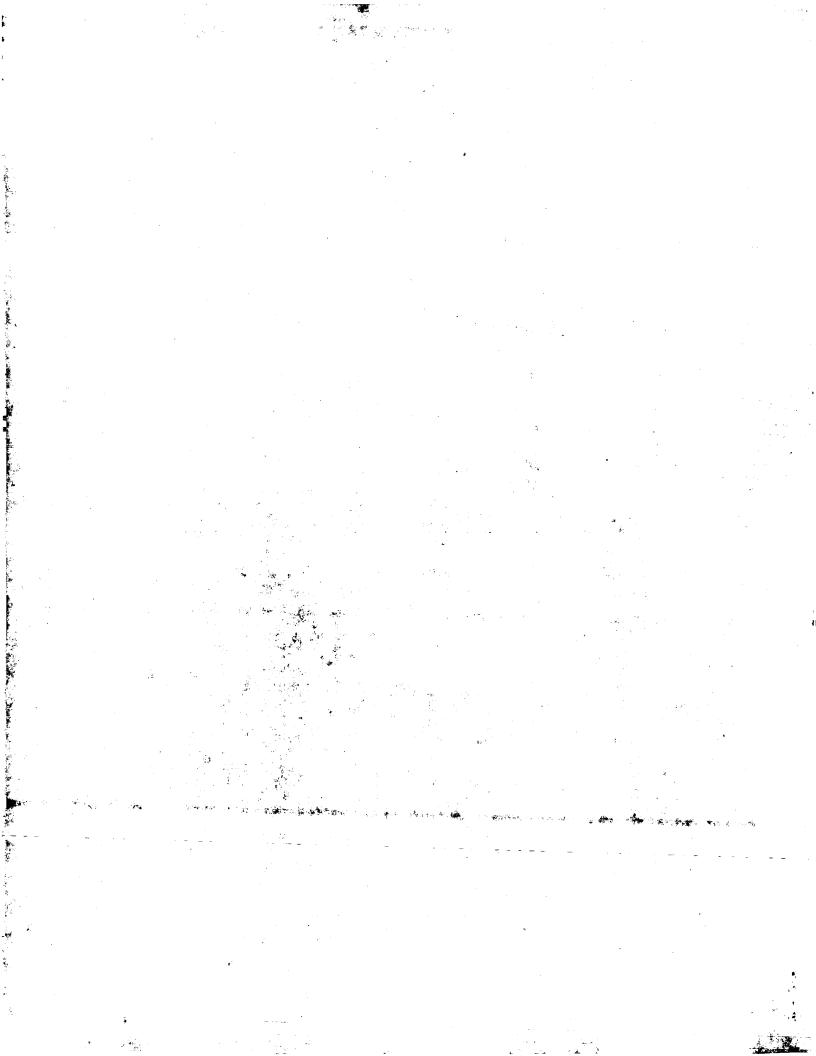
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478 CAGGTCATGATGATGGGCAGCGCCCGCGTGGCGGAGCTGCTGCTGCTCCACGGCGCGGAG 537
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Best Local Similarity 100.0%; Pred. No. 1.4e-50;
Matches 360; Conservative 0; Mismatches 0;
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Pred. No. 1.4e-50;
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Stone, 3., Jiang, P. and Kamb, A.
Mouse MTSI gene
Patent: US 5843756-A 5 01-DEC-
Location/Qualifiers
                           /organism="unknown"
343 c, 355 g
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Search completed: July 21, 2000, 06:05:24 Job time: 14858 sec
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Homo sapiens
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Homo saptens cyclin-dependent kinase inhibitor 2B (CDKN2B) gene,
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Skolnick,M.H., Cannon-Albright,L.A. and Kamb,A.
Germilne mutations in the MTS gene
Patent: US 5624819-A 5 29-APR-1997;
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43.0%; Score 360; DB 5; L
Best Local Similarity 100.0%; Pred. No. 1.4e-50;
Matches 360; Conservative 0; Mismatches 0;
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Sequence 5 from patent US
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141151.1 GI:2081741
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AF058758.1 GI:6808470
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                                                                                                     Calgary, 3330 Hospital Drive, N.W., Calgary, Alberta T2N 1N4,
Canada
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhin; Hominidae; Homo.
1 (bases 1 to 2147)
Murthy, S. K. and Demetrick, D.J.
Direct Submission
Submitted (09-APR-1998) Pathology and Oncology, University of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1839 GCGCTAGGCGCTITITICCCAGAAGCAATCCAGGCGCGCCGCTGGTTCTTGAGCGCAGG
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                                                                                                                                                                                                                                                                                                                    /gene="CDKN2B"
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/gene="CDKN2B"
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/db_xrsf="G1:6808471"
/translation="MREENGMPSGGS"
495 c 512 g 551 t
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                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="9"
/map="9p21"
                                                                                                                                                                     Location/Qualifiers
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R 14-APR-1994; US-346812.

R 14-SED-1994; US-346812.

R 14-SED-1994; US-346817.

R 29-NOV-1994; US-346817.

R 29-NOV-1994; US-346817.

R 29-NOV-1994; US-34681.

R 20-34681.

R 20-34681.

R 30-34681.

R 30-3
                                                                                                                                                                                                                                                                                                                                                                                      Cell-cycle regulatory protein p15 cDNA.
Cell-cycle regulatory protein p15; cyclin-dependent kinase inhibitor; CCR; gene therapy; transgenic animal; cancer; cell proliferation; ss; ds.
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Pred. No. 4.1e-165;
0; Mismatches 9;
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98.68;
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Copyright (c) 1993 - 2000
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T100745;
08-MAY-1996 (first entry),
Multiple tumour suppressor 2 (MTS2) gene ORF.
Multiple tumour suppressor; MTS2; cancer; diagnosis; assay;
predisposition; melanoma; leukaemia; lymphoma; prognosis;
panorreas; breast; thyroid; open reading frame; ORF; ds.
Homo sapiens.
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WPI; 95-344626/44.
P-PSDB; R81702.
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18-MAR-1994; US-215087.
18-MAR-1994; US-215086.
14-APR-1994; US-227369.
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Disclosure; Pages 102-103; 148pp; English.

An individual can be diagnosed as having a predisposition to cancer by detecting an alteration in the wild type multiple tumour suppressor (MTS) gene, using gene probes which hybridise to the MTS2 gene ORF T00745 (which encodes R81702). The above assay can also be used in the diagnosis and prognosis of melanoma, lymphoma, leukaemia and pancreas, breast and thyroid cancers, etc.
sequence 751 BP; 130 A; 225 C; 292 G; 104 T;
                                                                                                                                                Gaps
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                                                                                                                       Length 751;
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Human multiple tumour suppressor polypeptide, MTS2 encoding
                                                                                                                                                Indels
                                                                                                                      Score 677.2; DB 1;
Pred. No. 8.4e-137;
); Mismatches 8;
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Best Local Similarity 97.9%;
Matches 730; Conservative C
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Disclosure; Columns 75-78; 72pp; English.
The present sequence the human multiple tumour suppressor gen (MTS2), useful in cancer diagnosis.
Sequence 751 BP; 130 A; 225 C; 292 G; 104 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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Human multiple tumour suppressor gene 2.

Human; multiple; tumour; suppressor; MTS2;

Homo sapiens.
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335. .751
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18-MAR-1994; US-215086.
18-MAR-1994; US-215087.
14-APR-1994; US-215087.
17-MAR-1995; WS-251938.
17-MAR-1995; WS-251937.
17-MAR-1995; WS-474177.
(MYRI-) MYRIAD GENETICS INC.
(UTAH ) UNIV UTAH RES FOUND.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Multiple tumour suppressor; El-alpha; diagnosis; cancer; leukaemia; astrocytoma; glioblastoma; Hodgkin's lymphoma; melanoma; glioma; gene therapy; chronic; ds. Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wild-type multiple tumour suppressor (MTS) gene and mutant sequenc - useful in diagnosis, prognosis and therapy of human cancer, e.g. melanoma or leukaemia
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Pred. No. 8.4e-137;
0; Mismatches 8;
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                                                                                                            Location/Qualiflers
335. .751
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ilarity 97.9%;
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18-MAR-1994; US-215087.
14-APR-1994; US-227369.
01-JUN-1994; US-251938.
(MYRI-) MYRIAD GENETICS INC.
                                                                                                                                                                                                                                                                                              18-MAR-1994; US-214581.
18-MAR-1994; US-214582.
18-MAR-1994; US-215086.
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Best Local Similarity
Matches 730; Conserv
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                                                                                                                           cancer;
MLM; predisposition;
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                                                                                          AAAAGCCCGGAGCTAACGACCGGCCGCTCGGCCACTGCACGGGGCCCCAAGCCGC---AG
                         GGAGCAGCGTGGGAAAGAAGGGAAGAGTGTCGTTAAGTTTACGGCCAACGGTGGATTATC
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                                                                                                                                                                                                                     AGCCCAACTGCGCAGACCCTGCCACTCTCACCCGACCGGTGCATGATGCTGCCCGGGAGG
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                                                                                                                   GGGGCGGCAGCGATGAGGGTCTGGCCA---CGCCGGCGCGGGGACTAGTGGAGAAGGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kamb A;
WPI; 98-250421/22.
P-PSDB; W40526.
WAN specific for Multiple Tumour Suppressor IEI-beta gene -
useful for the diagnosis of cancers related to MTSIEI-beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            suppressor"
                                                                                                                                                                                                                                                                                                                                                                                                        Human MTS2 cDNA.
MTS2; multiple tumour suppressor; diagnosis;
germ-line mutation; familial melanoma locus;
Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag= a
/product= MTS2
/note= "multiple tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
335. .751
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                                                                                                                                                                                                                                                                                                                                                                                 standard; cDNA; 751
                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US5739027-A.
14-APR-1998.
07-JUN-1995; US-487033.
07-JUN-1995; US-214882.
18-MAR-1994; US-215086.
18-MAR-1994; US-215086.
14-APR-1994; US-227569.
01-JUN-1994; WS-255938.
                                                                                                                                                                                                                                                                                                                                                                                        V11250;
15-JUL-1998
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mutation(s) and their treatment
Disclosure; Fig 11; 72pp; English.
This cDNA sequence encodes a human multiple tumour suppression protein,
MTS2. The MTS gene locus is also referred to as the familial melanoma
(MLM) gene locus, located on human chromosome 9p21. Germ line mutations
(MLM) genes can be used in the diagnosis of predisposition to cancers,
e.g. melanoma, leukaemia, astrocytoma, gliboblastoma, lymphoma, glioma,
Hoddykin's lymphoma, CLL, and cancers of the pancreas, breast, thyroid,
ovary, uterus, testis, kidney, stomach and rectum.
Sequence 751 BP; 130 A; 225 C; 292 G; 104 T;
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                                                                                                                                            Length 751,
                                                                                                                                                                    Indels
                                                                                                                                            Score 677.2; DB 1;
Pred. No. 8.4e-137;
0; Mismatches 8;
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97.9%;
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Matches 730; Conservative
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This is the nucleotide sequence of the multiple tumour suppressor

This is the nucleotide sequence of the multiple tumour suppressor

(MTSIEIS) gene, used in the method of the invention. The MTS gene

(Is useful in the diagnosis and prognosis of human cancer, e.g. by

standard nucleic hybridisation techniques, of patient samples. The

mutated sequences are those that are present in somatic mutations

(C) of the gene in cancers. The vectors can be used for gene therapy

strategies to replace function of mutated protein in patients. These

can also be used to construct protein mimtatics, also for therapeutic

strategies. In addition the expression constructs can also be used

for recombinant production of MTS. Recombinant MTS can also be used

for recombinant production of MTS. Recombinant MTS can be used to

screen for drugs to be used for cancer therapy, and the protein

strategies are also be used to restore MTS function in a cell.

Sequence 751 BP; 130 A; 225 C; 292 G; 104 T;
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                                                                                                                                                                                                                                                                       p-PSDB; W74553.

Worletc acids based on multiple tumour suppressor, MTS, sequences useful as hybridisation probes, primers and recombinant production of MTS in the diagnosis and treatment of cancers related to MTS
04-DEC-1998 (first entry)
Coding sequence 2 of the multiple tumour suppressor MTSIEIS.
Multiple tumour suppressor; MTSIEIS; human; cancer; hybridisation; somatic mutation; gene therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCGCTAGGCGCTTTTTCCCAGAAGCAATCCAGGCGCGCCCGCTGGTTCTTGAGCGCCCAGG
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Best Local Similarity 97.9%; Pred. No. 8.4e-137
Matches 730; Conservative 0; Mismatches 8
                                                            Location/Qualiflers
335. .751
/*tag= a
/product= "human MTSIEIS"
                                                                                                                                                                                                                                    (MYRI-) MYRIAD GENETICS INC
Kamb A;
                                                                                                          US5801236-A.
07-SEP-1998.
07-JUN-1995; US-480810.
07-JUN-1995; US-214582.
18-MAR-1994; US-215586.
18-MAR-1994; US-215586.
18-MAR-1994; US-215586.
01-JUN-1994; US-227569.
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                                                   Homo sapiens
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GGGGCGGCAGCGATGAGGGTCTGGCCAGCGCCGCGGGGGACTAGTGGAGAAGGTGC 425
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein.
                                                                                                           The present sequence encodes a human multiple tumour suppressor 2 (MTS2) protein. The sequence is homologous to the corresponding murine gene. Primers designed from the gene can be used to design primers to detect abnormalities i.e. polymorphisms which may predispose towards malignancies such as melanoma, leukaemla,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9 GAGGACTCCGCGACGCGTCCGCACCCTGCGGCCAGACGGGCTTTGAGCTCGGCTGCGTCC
                                                        1 GAGGACTCCGCGACG-GTCCGCACCCTGCGGCCAGAGCGGCTTTGAGCTCGGCTGCTTCC
                                                                                                                                                                                      AGCCCCAACTGCGCAGACCCTGCCACTCTCACCCGACCGGTGCATGCTGCTGCCCGGGAGG
                                                                                                                                                                                                                                                                 Mouse multiple tumour suppressor gene segment – useful for primer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cDNA encoding a human multiple tumour suppressor 2 (MTS2)
Human; multiple tumour suppressor 1 gene; MTS1; cancer; ds
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thyroid, pancreas, uterus and kidneys.
Sequence 751 BP; 130 A; 225 C; 292 G;
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Pred. No. 8.4e-137;
0; Mismatches 8;
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                                                                                                                                                                                                                                                                                                                                                                                                                ACCTGCGCACAGCCACGGGGACTGA 741
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/*tag= b
/note= "splice s
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Best Local Similarity 97.9%;
Matches 730; Conservative
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V70595;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MYRI-) MYRIAD GENETICS II
Jiang P, Kamb A, Stone S;
WPI; 99-044585/04.
P-PSDB; W80526.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-JUL-1995; US-508735,
07-JUN-1995; US-487033
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28-JUL-1995;
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099168;
07-MAY-1996 (first entry)
107-MAY-1996 (first entry)
Human MTS2 DNA including exon 2, intron 2 and part of intron 1.
Multiple tumour suppressor; B1-alpha; diagnosis; cancer; leukaemia;
astrocytoma; glioblastoma; Hodgkin's lymphoma; melanoma; glioma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           331 CCCAACTGCGCAGACCCTGCCACTCTCACCGGACCGGTGCATGATGCTGCCCGGGAGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGGGGTCGTCTCCCCGTGGACTTGGCCGAGGAGCGGGGCCACCGCGACGTTGCAGGGTAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            538 CCCAACTGCGCAGACCCTGCCACTCTCACCCGACCGGTGCATGATGCTGCCCGGGAGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-APR-1994; US-227369.
01-UNU-1994; US-251938.
01-UNU-1994; US-251938.
(UTAH ) UNIV UTAH RES FOUND.
Cannon-Albright LA, Kamb A, Skolnick MH;
WPI: 95-344626/44.
Detecting polymorphism associated with cancer pre:disposition - a Detecting polymorphism associated with cancer pre:disposition - therapy and drug screening therapy and drug screening Example 6; Page 96; 148pp; English.
                                                                                                                                                                                                                                 Example 6; Page 96: 148pp; English.

An individual can be diagnosed as having a predisposition to by detecting an alteration in the wild type multiple tumour suppressor (MTS) gene, using gene probes which hybridise to (T00741) of the MTS2 gene. The above assay can also be used idagnosis and prognosis of melanoma, lymphoma, leukaemia and panoreas, breast and thyroid cancers, etc. . 355 G; 260 T; Sequence 1244 BP; 279 A; 343 C; 355 G; 260 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1244;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43.0%; Score 360; DB 1; 1
100.0%; Pred. No. 6.2e-69;
tive 0; Mismatches 0;
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274. .580
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Best Local Similarity 100.
Matches 360; Conservative
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581. .124
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US-214581.
US-214582.
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28-SEP-1995.
17-MAR-1995; U
18-MAR-1994; U
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                                                                             119 AAAAGCCCGGAGCTAACGACCGGCCGCTCGGCACTGCACGGGGCCCCAAGCCGC---AG
                                                                                                                                                                                                                                                                                                                                                                                                                  306 CGGGCGCTGCGCGTCTGGGGGCTGCGGAATGCGGGGAGAACAAGGGCATGCCCAGTG
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T00741;
08-MAY-1996 (first entry)
Multiple tumour suppressor 2 (MTS2) gene exon 2 contg. fragment.
Multiple tumour suppressor; MTS2; cancer; diagnosis; assay;
predisposition; melanoma; leukaemia; lymphoma; prognosis;
pancreas; breast; thyroid; exon 2; ds.
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/label= exon 2
530. .1244
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28-SEP-1995.
17-MAR-1995; U03537.
18-MAR-1994; US-214582.
18-MAR-1994; US-215087.
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Matches 360; Conservative
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01-SEP-1998.
07-JUN-1995; 480810.
07-JUN-1995; US-480810.
                                                                                                                                Kamb A;
WPI; 98-250421/22.
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Human MTS2 genomic DNA including exon 2.
MTS1: multiple tumour suppressor; diagnosis; cancer; germ-line mutation; familial melanoma locus; MLM; predisposition; ds.
                                                                                                                            Example 6; Page 96; 156pp; English.

The cDNA sequences encoding several multiple tumour suppressor (MTS) polypeptides have been isolated and sequenced. This sequence includes hotron 2, exon 2 and part of intron 1 of the MTS polypeptide, MTSL MTS polypeptide-encoding cDNAs and mutants of these are useful for the diagnosis or prognosis of human cancer. Germ-line mutations of MTS CDNAs can be used for diagnosing predisposition to melanoma, leukaemia, astrocytoma, glioblastoma, lymphoma, glioma, Hodgkin's lymphoma, CLL and cancers of the pancreas, thyrold, ovary, uteras, testis, kidney, stomach and rectum. The wild-type gene is useful for gene therapy and MTS polypeptides may also be used for protein replacement therapy. Also the polypeptides or cells contg an altered MTS gene are useful for screening for potential cancer therapeutics.

Sequence 1244 BP; 279 A; 343 C; 355 G; 260 T;
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                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                              mutant sequences
                                                                                             (MTS) gene and mutant sequenc
therapy of human cancer, e.g.
                                                                                                                                                                                                                                                                                                                                                                      CAGGTCATGATGATGGGCAGCGCCCGCGTGGCGGAGCTGCTGCTCCTCCACGGCGCGGAG
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                                                                                                                                                                                                                                                                                                                     43.0%; Score 360; DB 1; Length 1244; 100.0%; Pred. No. 6.2e-69; tive 0; Mismatches 0; Indels
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/note= "Corresponds to exon 2 in V11240"
                                                                                           Wild-type multiple tumour suppressor - useful in diagnosis, prognosis and melanoma or leukaemia
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1. 273
/*tag= a
//number= 1
274. .529
/*tag= b
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                                                           (MYRI-) MYRIAD GENETICS INC
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18-MAR-1994; US-215086.
18-WAR-1994; US-215088.
18-WAR-1994; US-215087.
14-APR-1994; US-227569.
01-JUN-1994; US-251938.
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Best Local Similarity
                                                                                 95-344401/44
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                                                                    Kamb A;
WPI; 95
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V11241
AC V11241
DT 15-JUL
DE HUMBAN
KW FAMILI
KW FAMILI
KW FAMILI
KW FAMILI
FT INTRON
FT ET
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Useful for the diagnosis of cancers related to MTSIE1-beta mutation (s) and their treatment mutation (s) and their treatment bisclosure; Fig 7: 72pp; English.

This sequence encodes the human multiple tumour suppression protein, MTSI, exon 2. The MTS gene locus is also referred to as the familial melanoma (MLM) genes can be used in the diagnosis of predisposition to cancers, e.g. melanoma, leukaemla, astrocytoma, gliboblastoma, lymphoma, glioma, Hodgkin's lymphoma, CLL, and cancers of the pancreas, breast, thyrold, ovary, uterus, testis, kidney, stomach and rectum. Sequence 1244 BP; 379 A; 343 C; 355 G; 260 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  478 CAGGTCATGATGATGGGCAGCGCCCGCGTGGCGGAGCTGCTGCTGCTCCACGGCGCGCGGAG 537
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04-DEC-1998 (first entry)
Nucleotide sequence of the multiple tumour suppressor 2.
Nucleotide sequence of the multiple tumour suppressor 2.
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Local Similarity 100.0%; Pred. No. 6.2e-69;
hes 360; Conservative 0; Mismatches 0;
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/*tag= a
/note= "intron 1
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18-MAR-1994; US-214582.

18-MAR-1994; US-215086.

18-MAR-1994; US-215087.

14-APR-1994; US-227369.

01-UUN-1994; US-221938.

17-MAR-1995; WO-003316.

(MYRI-) MYRIAD GENETICS INC.
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Query Match
Best Local 3
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T02964
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                                                                                                                                                       mutation(s)

Disclosure: Fig 7A-7B; 73pp; English.

This is the nucleotide sequence of the multiple tumour suppressor 2

This is the nucleotide sequence of the invention. The MTS gene
is useful in the diagnosis and prognosis of human cancer, e.g. by

standard nucleic hybridisation techniques, of patient samples. The
nutated sequences are those that are present in somatic mutations
of the gene in cancers. The vectors can be used for gene therapy
strategies to replace function of mutated protein in patients. These
can also be used to construct protein minetics, also for therapeutic
strategies. In addition the expression constructs can also be used
to recombinant production of MTS. Recombinant MTS can be used to
correct for recombinant production of MTS. Recombinant MTS can be used to
screen for drugs to be used for cancer therapy, and the protein
ttself may also be used to restore MTS function in a cell.
Sequence 1244 BB; 279 A; 343 C; 355 G; 260 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          271 CAGGTCATGATGATGGGCCAGCGCCCGCGTGCGGAGCTGCTGCTGCTCCACGGCGCGCGGAG 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          597
                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                       WPI; 98-494842/42.

Worlate acids based on multiple tumour suppressor, MTS, sequences useful as hybridisation probes, primers and recombinant production of MTS in the diagnosis and treatment of cancers related to MTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAGGTCATGATGATGGCCAGCGCCCGCGTGGCGGAGCTGCTGCTGCTCCACGGCGCGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        538 CCCAACTGCGCAGACCCTGCCACTCTCACCCGACCGGTGCATGATGCTGCCCGGGAGGGC
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                                                                                                                                                                                                                                                                                                                                                                                 43.0%; Score 360; DB 1; Length 1244; 100.0%; Pred. No. 6.2e-69; Live 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "corresponds to the exon of V70585"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human multiple tumour suppressor 2 (MTS2) DNA fragment.
Human; multiple tumour suppressor 1 gene; MTS1; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                V70586 standard; DNA; 1244 BP
                                                                            (MYRI-) MYRIAD GENETICS INC. Kamb A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-FEB-1999 (first entry)
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274. .529
18-MAR-1994; US-214582.
18-MAR-1994; US-215086.
18-MAR-1994; US-215087.
14-APR-1994; US-227369.
01-UUN-1994; US-221338.
17-MAR-1995; WO-U03316.
                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 360; Conservative
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V70586
AC V70586
DT 03-FEB
DE Human 1
OS Homo 8
FFH Key
FFT intron
FT exon
FT exon
FT EY
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Cell-cycle requlatory protein p15 cDNA.
Cell-cycle requlatory protein p15; cyclin-dependent kinase inhibitor;
CCR; gene therapy; transgenic animal; cancer; cell proliferation;
ss; ds.
                                                                                                                                                                                       Example 6; Fig 7A-B; 80pp; English.

The present sequence represents part of intron 1, exon 2 and intron 2 for a human multiple tumour suppressor 2 (MTS2) gene. The MTS1 sequence is homologous to the corresponding murine gene. Primers designed from the gene can be used to design primers to detect abnormalities i.e. polymorphisms which may predispose towards malignancies such as melanoma, leukaemia, astrocytoma, lymphoma, glioma, as well as tumours of e.g. the breast, thyroid, pancreas,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    478 CAGGTCATGATGATGGGCAGCGCCCGCGTGCGGAGCTGCTGCTGCTCCACGGCGCGCGGAG 537
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                                                                                                                                                 - useful for primer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1244;
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                                                                                                                                                                                                                                                                                                                                                                                                                 355 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43.0%; Score 360; DB 1; I
100.0%; Pred. No. 6.2e-69;
tive 0; Mismatches 0;
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WPI; 95-373798/48.
                                                                                               Jiang P, Kamb A, Stone S;
WPI; 99-044585/04.
Mouse multiple tumour suppressor gene segment
                                                                                                                                                                                                                                                                                                                                                                                                                 343 C;
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14-APR-1995.
14-APR-1994; US-227371.
25-MAY-1994; US-248812.
29-NOV-1994; US-306511.
29-NOV-1994; US-346147.
(COLD-) COLD SPRING HARBOR LAB.
                                                                                                                                                                                                                                                                                                                                                                                                                 279 A;
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28-JUL-1995; 058735.
28-JUL-1995; US-508735.
07-JUN-1995; US-487033.
(MYRI-) MYRIAD GENETICS INC.
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Matches 360; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                      uterus and kidneys.
Sequence 1244 BP;
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Truncated p27/p16 fusion protein encoding DNA.
Truncated p27/p16 fusion protein encoding DNA.
Cyclin-dependent kinase. CDK; CDK/cyclin complex; inhibitory; restenosis; CDK-binding motif; endothelialisation; fusion protein; therapeutic; acne; intracellular; transcetlular; transcytosis; vascular wound; repair; hair; smooth muscle; cardiovascular; arterioscierctic; fibroric disorder; cellular proliferation; rheumatoid arthritis; diabetes; cirrhosis; graft; tumour; inflammation; neurodegeneration; periodontal; spermatogenesis; tachycardia; human; p27; p16; truncated; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     969
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                                                                                                                                                                                                                                                                                         337 GAGAACAAGGGCATGCCCAGTGGGGGGGGGGATGAGGGTCTGGCCACGCCGGCGCGG 396
                                                                                                                                                                                                                                                                                                                     GGACTAGTGGAGAAGGTGCGACACTCCTGGGAAGCCGGCGGGATCCCAACGGAGTCAAC 456
                                                                                                                                                                                                                                                               Gaps
            New cell cycle regulating proteins bind to cyclin dependent kinase and related nucleic acids, antibodies etc., used in diagnosis and therapy of abnormal cell proliferation, degeneration etc.
                                                                                                                                                                                                                                                                                                                                                                                                                          CATGATGCTGCCCGGGAGGCTTCCTGGACACGCTGGTGCTGCTGCTGCACCGGGCCGGGCG
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                                                                                                                                                                                                                                                               1;
                                                  Claim 43; page 81-82; 109pp; English Corollar Corollar Colling Corollar 43; page 81-82; 109pp; English Cond. (CR) Coding for the mouse cell-cycle regulatory (CCR) protein p15 (R85118) was isolated from an embryonal carcinomal library using a probe based on a mouse CCR p13.5 cDNA (T02965). The isolated cDNA can be used: to detect mutations in CCR genes that lead to cell proliferation; to breed transgenic animals to study cellular disorders involving CCR allele mutation/misexpression; and to correct CCR-deficient cells
                                                                                                                                                                                                                                  Length 580;
                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                Score 276.8; DB 1;
Pred. No. 3.7e-51;
0; Mismatches 97;
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29-JUL-1998: U15759.
29-JUL-1997: US-902572.
(MITO-) MITOTIX INC.
Beach DH, Gyuris J, Lamphere L;
                                                                                                                                                                                                                                Query Match
Best Local Similarity 77.9%;
Matches 346; Conservative 0
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                                                                                                                                                                                      109 A;
                                                                                                                                                                           (gene therapy).
Sequence 580 BP;
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WO9906540-A2.
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Fusion and chimaeric proteins including cyclin-dependent kinase
binding motif - used for regulation of cell proliferation and
liferentiation, for treatment of, e.g. vascular injury, cancers,
fibrosis and neurodegeneration

S claim 60: Page 85: 88pp; English.

Claim 60: Page 85: 88pp; English.

The invention relates to novel inhibitors of cyclin-dependent kinases
CCDKs), particularly CDKCyclin complexes. It provides a recombinant
transfection system (A) that comprises: (i) first gene construct
comprising a sequence encoding an inhibitory polypeptide containing at
lanked to a transcription regulator functional in eukaryotic cells; (ii)
second gene construct comprising a sequence encoding a polypeptide that
construct comprising a sequence encoding a polypeptide that
promotes endothelialisation, and (iii) a gene delivery composition for
delivering the GCs to a cell for transfection. Also provided are nucleic
collection sequence (TP) from an intracellular protein that alters a
cellular process when FP enters the cell, and (ii) a transcellular
polypeptide sequence (TP) from an intracellular protein that alters a
cellular process when FP enters the cell, and (ii) a transcellular
polypeptide sequence (TP) that promotes transcytosis of FP. The FP
consists of at least one CDK binding motif and a TP. See X26220 for
detailed uses of the recombinant transfection system.
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Truncated p27/p16 fusion protein encoding DNA.
Truncated p27/p16 fusion protein encoding DNA.
Cyclin-dependent kinase; CDK, CDK/cyclin complex; inhibitory; restenosis; CDK-binding motif; endothelialisation; fusion protein; therapeutic; acne; intracellular; transcellular; transcytosis; vascular wound; repair; hair;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          450
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            detailed uses of the recombinant transfection system. The present sequence represents a DNA encoding a human truncated \mathfrak{p}27/\mathfrak{p}16 fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 271 GGGGGTGGCGGTTCCGGCGGGGGGGTCCGTCGAGGATCCGGCGGCGGGGGAGCAGCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        658 TGGGGTCGTCTGCCCGTGGACTTGGCCGAGGAGCGGGGCCACCGCGACGTTGCAGGGTAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    331 GAGCCTTCGGCTGACTGGCTGGCCACGGCCGCGGGGTCGGGGTAGAGGAGGTGCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  418 CACTCCTGGGAAGCCGGCGCGGGATCCCAACGGAGTCAACCGTTTCGGGAGGCGCGCGATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 782;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   114 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tch 32.4%; Score 271.4; DB 1; al Similarity 77.6%; Pred. No. 5.4e-50; 342; Conservative 0; Mismatches 96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   295 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   236 C;
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Threates and neurodegeneration of the control of th
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smooth muscle; cardiovascular; arteriosclerotic; fibrotic disorder;
cellular proliferation; rheumatoid arthritis; diabetes; cirrhosis; graft;
tumour; inflammation; neurodegeneration; periodontal; spermatogenesis;
tachycardia; human; p27; p16; truncated; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      478 CAGGICAIGAIGAIGAGGCCCCCCCCGCGIGCGGAGCIGCIGCIGCICCACGCCGCGCGGGG 537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         801
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                                                                                                                                                                                                                                                                                                              Fusion and chimmeric proteins including cyclin-dependent kinase binding motif - used for regulation of cell proliferation and differentiation, for treatment of, e.g. vascular injury, cancers,
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                                                                                                                                                                                                                                                             Beach DH, Gyuris J, Lamphere L; WPI; 99-153770/13.
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                                                                                                                                                       11-FEB-1999.
29-JUL-1998; U15759.
29-JUL-1997; US-902572.
(MITO-) MITOTIX INC.
                                                                                                         Homo sapiens
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Search completed: July 21, 2000, 06:18:48 Job time: 13645 sec Appli Appli

Title: Perfect score:

Sequence:

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Run on:

Scoring table:

Searched:

Database :

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Sequence 45, Ale
Sequence 3, Ale
Sequence 3, Ale
Sequence 1, Ale
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APPLICANT: Beach, David H.
APPLICANT: Demetrick, Douglas J.
APPLICANT: Demetrick, Douglas J.
APPLICANT: Hannon, Gregory J.
TITLE OF INVENTION: Related Thereto
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 837;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 837; DB 4; 1
Pred. No. 3.4e-179;
US-08-480-810-1
US-08-848-735-1
US-08-448-047-1
US-09-115-2120-1
US-09-115-212-1
US-08-474-177-36
US-08-474-177-36
US-08-480-810-36
US-08-508-735-36
US-08-848-251-36
US-08-120-130-36
US-09-120-130-36
US-08-135-36
US-08-138-38-1
US-08-508-735-45
US-08-508-735-45
US-08-508-735-45
US-08-130-130-36
US-08-135-35-36
US-08-135-35-36
US-08-138-38-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 0210

ZIP: 0210

ZIP: 0210

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII(text)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/306,511A

FILING DATE: 14-SEP-1994

ATYONEY/AGENT INFORMATION:

NAME: Vincent, Matthew P.

REGISTRATION NUMBER: 36,709

REGISTRATION INFORMATION:

TELEPAN: (617) 227-7400

TELEPAN: (617) 227-7400

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 837 base pairs

LENGTH: 837 base pairs

LENGTH: 11near
                                                                                                                                                                                                                                                                                    ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                     Sequence 3, Application US/08306511A Patent No. 5962316
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100.0%;
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Best Local Similarity
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; LOCATION:
US-08-306-511A-3
                                                                                                                                                                                                                                                                                                                           RESULT 1
US-08-306-511A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: BOS
STATE: MA
COUNTRY:
  July 21, 2000, 06:06:23 ; Search time 86.37 Seconds (without alignments) 1333.035 Million cell updates/sec
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                                                                                                                                                                         1 GAGGACTCCGCGACGGTCCG......AGGCTGCCAACGGGGAGCGG 837
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Sequence 15,
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Sequence 5,
Sequence 5,
Sequence 5,
Sequence 5,
Sequence 5,
Sequence 7,
Sequence 7,
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                                                                                                                                                                                                                                                                                                                                                                                         GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-306-511A-3
US-08-893-274-3
US-08-627-610-3
US-08-581-918A-3
PCT-US95-04636-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-474-177-15
US-08-487-033-15
US-08-508-735-15
US-08-508-735-15
US-08-78-135-15
US-08-78-135-15
US-08-78-135-15
US-09-115-252-15
US-09-115-252-15
US-08-487-177-5
US-08-480-810-5
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US-08-474-177-1
US-08-487-033-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                                  nucleic search, using sw model
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837
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Maximum DB seq length: 1000000
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Match Length
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Score

Result No.

8112.8 8812.8 8112.8 877.2 6777.2 6777.2 877

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61 CGCTAGGCGCTTTTTCCCAGAAGCAATCCAGGCGCCCCCCCTGGTTCTTGAGCGCCAGGA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIV-071.09
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 832-1000
TELEFAX: (617) 832-7000
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 837 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/893,274
CLASSIPECATION: 800
CLASSIPECATION: 800
PRIOR APPLICATION: 800
PRIOR APPLICATION NUMBER: US 08/306,511
FILING DATE: 14-SEPTEMBER-1994
PRIOR APPLICATION NUMBER: US 08/248,812
FILING DATE: 25-MAY-1994
PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/227,371
RIGHT DATE: 14-APRIL-1994
PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/154,915
FILING DATE: 18-NOVEMBER-1993
PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/991,997
FILING DATE: 17-DECEMBER-1992
PRIOR APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-OCTOBER-1992
PRIOR APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-OCTOBER-1992
ATTORNEY/AGENT INFORMATION: NAME: VAICHMEN P.
REGISTRATION NUMBER: 36,709
                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
  One Post Office Square
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 100. Matches 837; Conservative
                                                                             ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                       Boston
                                                              USA
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; LOCATION:
US-08-893-274-3
                                       STATE: MA
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                                                                                                                                        61 CGCTAGGCGCTTTTTCCCAGAAGCAATCCAGGCGCCCCCCCTGGTTCTTGAGCGCCCAGGA 120
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                                                            AAAGCCCGGAGCTAACGACCGGCCGCTCGGCACTGCACGGGGCCCCCAAGCCGCAGAAGAA
                                                                                                                                                                                                                                                                                                                                                                  AGCAGCGTGGGAAAGAAGGGAAGAGTGTCGTTAAGTTTACGGCCAACGGTGGATTATCCG
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  0; Indels
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Petent No. 5568821
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Beach, David H.
APPLICANT: Bearano, Manuel
APPLICANT: Serrano, Manuel
APPLICANT: GENTANO, GENTANO, GENTANO, GENTANO, GENTANO, GENTANO, GENTANO, TITLE OF INVENTION: and USes Related Thereto
WUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELIOT LLP
  0; Mismatches
Matches 837; Conservative
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US-08-893-274-3
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Length 837 0; Indels 09

241 AGCAGCGTGGGAAAGAAGGGAAGAGTGTCGTTAAGTTTACGGCCAACGGTGGATTATCCG 300

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Patent No. 5919997
GENERAL INFORMATION:
APPLICANT: Beach, David H.
APPLICANT: Serrano, Manuel
APPLICANT: Definho, Ronald A.
TITLE OF INVENTION: Transgenic Animals Having Modified Cell-Cycle
TITLE OF INVENTION: Regulation
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                         781 TACCCAATTTCCCACCCCACCTAATTCGATGAAGGCTGCCAACGGGGAGCGG 837
                                                                                                                                                     TCCTGGGAAGCCGGGGGTCCCAACGGAGTCAACCGTTCGGGAGGCGCGCGATCCAG
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                             GGCCGCTGCGCGTCTGCGGGGCTGCGGAATGCCGGAGAGGAGAACAAGGGCATGCCCAGTGGG
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                                                                                                                                                                                                        COUNTY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBW PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION: 800
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: CSI-001CP6
TELECOMMUNICATION: NUMBER: CSI-001CP6
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STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: USA
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US-08-627-610-3
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Pred. No. 8.8e-174;
0; Mismatches 7;
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98.8%;
TELEFAX: (617) 227-5941
INFORMATION FOR SEG ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 850 base pairs TYPE: nucleic acid STRANDEDNESS: both TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                             Query Match
Best Local Similarity 98.8
Matches 830; Conservative
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US-08-627-610-3
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PERSILT 4 NAPLICATION US/08581918A
PERENT NO. 6043001
PERSILT A MAPLICATION US/08581918A
PERSILT NO. 6043001
PERSILT NORMATION:
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Score 812.8; DB 5; Length 850; Pred. No. 8.8e-174;

97.18; 98.88;

Query Match Best Local Similarity

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CGCTAGGCGCTTTTTCCCAGAAGCAATCCAGGCGCGCCGCTGGTTCTTGAGCGCCAGGA 120
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                             GAGGACTCCGCGACGGTCCGCACCCTGCGGCCAGAGCGGCTTTGAGCTCGGCTTCCCG
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  Mismatches
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CURRENT APPLICATION DATA:
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PCT-US95-04636-3
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                                                                                                                                                                                                                                                      TGGGGTCGTCTGCCCGTGGACTTGGCCGAGGAGCGGGGCCACCGCGACGTTGCAGGGTAC
Sequence 15, Application US/08474177
Patent No. 5624819
GENERAL INFORMATION:
APPLICANT: Skolnick, Mark H.
APPLICANT: Kamb, Alexander
TITLE OF INVENTION: GERMLINE MUTATIONS IN THE MTS GENE
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Venable, Baetjer, Howard & Civiletti, STREET: 1201 New York Avenue, Suite 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTAM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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FILING DATE: 07-JUN-1995
CLASSIPICATION 435
CLASSIPICATION ATA:
APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/03537
FILING DATE: 17-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,938
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,086
FILING DATE: 18-MAR-1994
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,086
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION D
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APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-MAR-1994
ATTORNEY/AGENT INFORMATION:
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REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24
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MEDIUM TYPE: Floppy disk
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LENGTH: 751 base pairs
TYPE: nucleic acid
STRANBEDNESS: double
TOPOLOGY: linear
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                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/346,147
FILING DATE: 29-NOV-1994
PRIOR APPLICATION NUMBER: US 08/306,511
FILING DATE: 14-SEP-1994
PRIOR APPLICATION NUMBER: US 08/248,812
FILING DATE: 25-MAY-1994
PRIOR APPLICATION NUMBER: US 08/248,812
FILING DATE: 15-MAY-1994
PRIOR APPLICATION NUMBER: US 08/227,371
FILING DATE: 14-APR-1994
INFORMATION FOR SEQ 1D NO: 3:
FECULATION FOR SEQ 1
PCT/US95/04636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 850 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDS
338..751
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PCT-US95-04636-3
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Best Local S
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                                                                                                                                                                                     Query Match 80.9%; Score 677.2; DB 1; Length 751; Best Local Similarity 97.9%; Pred. No. 1.8e-143; Matches 730; Conservative 0; Mismatches 8; Indels 8.
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US-08-487-033-15
Sequence 15, Application US/08487033
Patent No. 5738027
SENERAL INFORMATION:
                                                                 ORGANISM: Homo sapiens
                                                                                                NAME/KEY: CDS
LOCATION: 335..751
MOLECULE TYPE: C
HYPOTHETICAL: NC
ANTI-SENSE: NO
ORIGINAL SOURCE:
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US-08-474-177-15
                                                                                   FEATURE
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                                                                                           ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP STREET: 1201 New York Avenue, Suite 1000
                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,033 FILING DATE: 07-JUN-1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 80.9%; Score 677.2; DB 2; Best Local Similarity 97.9%; Pred. No. 1.8e-143; Matches 730; Conservative 0; Mismatches 8;
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REGISTRATION NUMBER: 28,957
REGISTRATION NUMBER: 24884-109348-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
                                                                                                                                                                                                                                                                                                                                                                                                                                          PRICE APPLICATION TO THE PRICE APPLICATION NUMBER: PCT/US95/03316 FILING DATE: 17-MAR-1995
PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/251,938 FILING DATE: 01-JUN-1994
PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/215,087 FILING DATE: 18-MAR-1994
PRIOR APPLICATION NUMBER: US 08/215,086 FILING DATE: 18-MAR-1994
PRIOR APPLICATION NUMBER: US 08/215,086 FILING DATE: 18-MAR-1994
PRIOR APPLICATION NUMBER: US 08/215,086 FILING DATE: 18-MAR-1994
APPLICANT: Kamb, Alexander
TITLE OF INVENTION: WYSIE1-Beta GENE
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 08/227,369
FILING DATE: 14-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-MAR-1994
ATTOREY/AGENT INFORMATION:
                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: double
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LOCATION: 335..751
                                                                                                                                            Washington
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US-08-487-033-15
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CITY: Wa
STATE: D
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                                                                                  AAAAGCCCGGAGCTAACGACCGGCCGCTCGG-CACTGCACGGGGCCCCCAAGCCGCAGAAG
          596 GCTTCCTGGACACGCTGGTGGTGCTGCACCGGGCCGGGGCGCGGGCTGGACGTGCGCGATG
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                                         416 GACACTCCTGGGAAGCCGGCGCGGATCCCAACGGAGTCAACCGTTTCGGGAGGCGCGCGA
                                                                                                                                                                                                                                                          476 TCCAGGTCATGATGATGGCCAGCGCCGCGTGGCGGAGCTGCTGCTGCTCCACGGCGCGG
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                                                                                                                                                                       GGGCGCCAGCGATGAGGGTCTGGCCA---CGCCGGCGCGGGGGACTAGTGGAGGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Alexander
TITLE OF INVENTION: MTS1 GENE
NUMBER OF SEQUENCES: 36
CORRESPONDERE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
CITY: Washington
STATE: DC
COUNTRY: USA
IP: 2006
COMPUTRY: USA
ZIP: 2006
KEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,810
FILING DATE: 07-7UN-1995
CLASSIFICATION 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/03316
FILING DATE: 17-MAR-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 15, Application US/08480810 Patent No. 5801236 GENERAL INFORMATION:
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60 GCGCTAGGCGCTTTTTCCCAGAAGCAATCCAGGCGCGCCCGCTGGTTCTTGAGCGCCCAGG 119
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                                                                               APPLICATION NUMBER: US 08/215,08/
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/215,086
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,369
FILING DATE: 14-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Inhen, Jeffrey L.
REGISTRATION NUMBER: 28,957
RECISTRATION NUMBER: 28,957
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 751 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
01-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
                         PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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; LOCATION:
US-08-480-810-15
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                CCTGGGGTCGTCTGCCCGTGGACTTGGCCGAGGAGCGGGCCCACCGCGACGTTGCAGGGT
                                                             AGCCCAACTGCGCAGACCCTGCCACTCTCACCCGACCGGTGCATGCTGCTGCCCGGGAGG
                                                                                                                                                                                                                                                                                                                                                             Sequence 15, Application US/08508735
Patent No. 5843756
GENERAL INFORMATION:
APPLICANT: Stone, Steven
APPLICANT: Jiang, Ping
APPLICANT: Kamb, Alexander
TITLE OF INVENTION: MTS GENE AND THERAPEUTIC USE THEREOF
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/508,735
FILING DATE:
CLASCOMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US to be assigned
FILING DATE: 07-JUN-1995
PRIOR APPLICATION NUMBER: PCT/US95/03316
FILING DATE: 17-MAB-1995
ATTORNEY/AGENT INFORMATION:
NAME: Inhen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24884-109348
TELECOMMUNICATION:
                                                                                                                                                                                                                                                       716 ACCTGCGCACAGCCACGGGGGACTGA 741
                                                                                                                                                                                                                                                                         ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 751 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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COMPUTER READABLE FORM:
MEDIUM TYPE: Flore
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STATE: DC
COUNTRY: USA
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                                                                                                   Length 751;
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                                                                                                   DB 3;
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                                                                                                 Score 677.2; DB 3;
Pred. No. 1.8e-143;
0; Mismatches 8;
          COCATION: 335..751
FEATURE:
NAME/RES:
LOCATION: 490..491
UCHER INFORMATION: /note- "Splice site"
US-08-508-735-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     716 ACCTGCGCACAGCCACGGGGGACTGA 741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Skolnick, Mark H. APPLICANT: Cannon-Albright, Lisa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 15, Application US/08848251

Patent No. 5999815

GENERAL INFORMATION:

APPLICANT: Skolnick, Mark H.
                                                                                                 Query Match 80.9%;
Best Local Similarity 97.9%;
Matches 730; Conservative
CDS
335..751
NAME/KEY:
LOCATION:
FEATURE:
NAME/KEY:
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US-08-848-251-15
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120 AAAAGCCCGGAGCTAACGACCGGCCGCTCGG-CACTGCACGGGGCCCCAAGCCGCAGAAG
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US-08-486-047-15
Sequence 15, Application US/08486047
Sequence 15, Application US/08486047
GENERAL INFORMATION:
APPLICANT: Kamb, Alexander
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
CITY: Washington
STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 20005
ZIP: 20005
COMPUTER READABLE FORM:
MEDIOW TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,047
FILLING DATE: O7-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  716 ACCTGCGCACAGCCACGGGGGACTGA 741
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TITLE OF INVENTION: GERMILINE MUTATIONS IN THE MTS GENE AND TITLE OF INVENTION: GERMILINE MUTATIONS IN THE MTS GENE AND TITLE OF INVENTION: GENE MUTATION TO CANCER AT THE MTS TITLE OF INVENTION: GENE NUMBER OF SEQUENCES: 36 CORRESPONDENCE ADDRESS: ADDRESSE: Venable Property STREET OF STREET OF STREET OF STREET.
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                                                                                                                          STREE: Venable, Baetjer, Howard & Civiletti, LLP STREET: 1201 New York Avenue, Suite 1000 STATE: DC COUNTRY: USA
                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CORFURE: The PC compatible
CORFURE: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin DATA:
APPLICATION NUMBER: US/08/448,251
FILING DATE: US/08/44,083
FILING DATE: 17-MAR-1995
APPLICATION NUMBER: US 08/251,938
FILING DATE: 01-UN-1994
PRIOR APPLICATION NUMBER: US 08/251,938
FILING DATE: 18-MAR-1994
PRIOR APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-MAR-1994
PRIOR APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-MAR-1994
PRIOR APPLICATION NUMBER: US 08/215,086
FILING DATE: 18-MAR-1994
PRIOR APPLICATION NUMBER: US 08/217,369
FILING DATE: 18-MAR-1994
APPLICATION NUMBER: US 08/217,369
FILING DATE: 18-MAR-1994
PRIOR DATE: 18-MAR-1994
PRIOR DATE: 18-MAR-1994
ATTORNEY AGENT INFORMATION:
NAME: INFORMATION:
NAME: INFORMATION:
NAME: VACENT NUMBER: 24/814,582
FILING DATE: 2202-962-4810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 15: SEQUENCE CHARACTERISTICS: LENGTH: 751 base pairs TYPE: nucleic soid STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 202-962-8300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: 11near
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; LOCATION:
US-08-848-251-15
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GCTTCCTGGACACGCTGGTGGTGCTGCACCGGGCCGGGGGCGCGGCTGGACGTGCGCGATG 655
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             416 GACACTCCTGGGAAGCCGGCGGGGATCCCAACGGAGTCAACCGTTTCGGGAGGCGCGCGA 475
                                                                                                                                                                                                                        ADDRESSEE: Venable, Baetjer, Howard & Civiletti, STREET: 1201 New York Avenue, Suite 1000 STREET: DC STATE: DC COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/120,130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Ihnen, Jeffrey L.
REGISTRATION UNDRER: 28,957
REFERENCE/DOCKET UNMBER: 24884-109348
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RILING DATE: 18 WAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,086
FILING DATE: 18 WAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,369
FILING DATE: 14 APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/214,582
FILING DATE: 18 WAR-1994
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,938
FILING DATE: 01-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,087
                                                                                                                                                                                                                                                                                                                                       716 ACCIGCGCACAGCCACGGGGACTGA 741
                                                                                                                                                                                                                                                                                                                                                        Sequence 15, Application US/09120130; Patent No. 6037462.
GENERAL INFORMATION:
APPLICANT: Kamb, Alexander
ITLE OF INVENTION: MTS1 GENE
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/480,810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 20005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120 AAAAGCCCGGAGCTAACGACCGGCCGCTCGG-CACTGCACGGGGCCCCAAGCCGCAGAAG 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGAGCAGCGTGGGAAAGAAGGGAAGAGTGTCGTTAAGTTTACGGCCAACGGTGGATTATC 298
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Pred. No. 1.8e-143;
0; Mismatches 8;
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PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/03316
FILING DATE: 17-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,938
FILING DATE: 01-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,086
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,369
FILING DATE: 14-APR-1994
PRIOR APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-MAR-1994
ATORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 28,957
REFERENCE/TOCKET NUMBER: 28,957
RELEPHONE: 202-962-8300
TELEFRAX: 202-962-8300
                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 15: SEQUEDNCE CHARACTERISTICS: LENGTH: 751 base pairs TYPE: nucleic acid STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80.9%;
97.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 730; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDS
335..751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION:
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Score 677.2; DB 5; Length 751; Pred. No. 1.8e-143;
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                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
GURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/115,252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Thnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
FREERENCE/DOCKET NUMBER: 24884-109348
TELECHONE: 202-962-4810
                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/480,810
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: PCT/US95/03316
FILING DATE: 17-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,938
FILING DATE: 01-JUN-1994
PRIOR APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-MAR-1994
PRIOR APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 08/215,086 FILING DATE: 18 MAR-1994 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,369 FILING DATE: 14-APR-1994
             726 ACCTGCGCACAGCCACGGGGGACTGA 751
                                                                                          Sequence 15, Application US/09115252
Patent No. 6060301
GENERAL INFORMATION:
APPLICANT: Kamb, Alexander
TITLE OF INVENTION: MTSI GENE
NUMBER OF SEQUENCES: 36
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97.9%;
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 751 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                               CORRESPONDENCE ADDRESS: ADDRESSE: Venable,
                                                                                                                                                                                                                                                                                           ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; LOCATION:
US-09-115-252-15
                                                            RESULT 13
US-09-115-252-15
                                                                                                                                                                                                                                                                           COUNTRY:
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Pred. No. 1.8e-143;
0; Mismatches 8;
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TELEPHONE: 202-962-4810
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 751 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-CENET
                                                                                                                                                                                                                                                                                                                              80.9%;
97.9%;
                                                                                                                                                                                           ORIGINAL SOURCE:
ORGANISM: Homo saplens
                                                                                                                                                                                                                                                                                                                            Query Match 80.9
Best Local Similarity 97.9
Matches 730; Conservative
                                                                                                                                                                                                                                               CDS
335..751
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                                                                                                                                                                                                                                            ; NAME/KEY:
; LOCATION:
US-09-120-130-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      416
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658 IGGGGTCGTCTGCCCGTGGACTTGGCCGAGGAGCGGGGCCACCGCGCGACGTTGCAGGGTAC 717
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    598 ITCCTGGACACGCTGGTGGTGCTGCACCGGGCCGGGGCGCGGCTGGACGTGCGGATGCC 657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          538 CCCAACTGCGCAGACCCTGCCACTCTCACCCGACCGGTGCATGCTGCTGCCGGGAGGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Corresponds to exon of ID NO:4"
                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43.0%; Score 360; DB 1; L. 100.0%; Pred. No. 1.7e-72; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24884-109348-E
                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,938
FILING DATE: 01-0UN-1994
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,086
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,369
FILING DATE: 14-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-MAR-1994
ATTORNEY AGGENT INFORMATION:
NAME: INHEN, JOHNEY ENGISTRATION NUMBER: 28,957
REGISTRATION NUMBER: 28,957
                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/03537
FILING DATE: 17-MAR-1995
                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,177
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 24
TELECHANTION INFORMATION
TELECHANE: 202-962-4810
TELEFAX: 202-962-830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
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Matches 360; Conservative
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TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCATION: 274..529 CTHER INFORMATION: OTHER INFORMATION: US-08-474-177-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_RNA
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                                                                                                                          60 GCGCTAGGCGCTTTTTCCCAGAAGCAATCCAGGCGCGCCCGCTGGTTCTTGAGCGCCCAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
CITY: Washington
  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         716 ACCTGCGCACAGCCACGGGGGACTGA 741
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APPLICANT: Cannon-Albright, Lisa
APPLICANT: Kamb, Alexander
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Matches 730; Conservative
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STATE: DC
COUNTRY:
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                                                    718 CTGCGCACACCCACGGGGGACTGACGCCAGGTTCCCCAGCCGCCCACAACGACTTTATTT
                                                                                                                                                                                         US-08-487-033-5

US-08-487-033-5

Sequence 5, Application US/08487033

Patent No. 5739027

Patent No. 5739027

PAPLICANT: Ramb, Alexander

TITLE OF INVENTION:

MYSIEL-Beta GENE

CORRESPONDENCE: 36

CORRESPONDENCE: 36

CORRESPONDENCE: Venable, Baetjer, Howard & Civiletti, LLP

STREET: 1201 New York Avenue, Suite 1000

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP
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MEDIUM TYPE: I Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: BW PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,033
FILING DATE: 07-JUN-1995
CLASSIFICATION NUMBER: PCT/US95/03316
FILING DATE: 17-MAR-1995
FILING DATE: 01-JUN-1994
FRIOR APPLICATION NUMBER: US 08/215,087
FILING DATE: US 08/215,087
FILING DATE: US 08/215,087
FILING DATE: US 08/215,087
FILING DATE: US 08/215,086
FILING DATE: US 08/215,086
FILING DATE: US 08/215,086
FILING DATE: US 08/215,086
FILING DATE: US 08/214,582
FILING DATE: US 08/214,583
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                                                                                                                                                                    Length 1244;
                                                                                                                                                                    Query Match 43.0%; Score 360; DB 2; Length 12 Best Local Similarity 100.0%; Pred. No. 1.7e-72; Matches 360; Conservative 0; Mismatches 0; Indels
| LOCATION: 1..273
| FEATURE: | INSC.RNA
| LOCATION: 274..529
| OTHER INFORMATION: ID NO:4" | Corresponds to exon of SEQ
| US-08-487-033-5
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               GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                         OM nucleic - nucleic search, using sw model
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837
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em_est2:**
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Perfect score:
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118: gb_gss14:*
119: gb_gss15:*
120: gb_gss15:*
121: gb_gss17:*
122: gb_gss18:*
123: gb_gss18:*
124: em_gss13:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	ion	94605	28496 ds02h12	71381 wl81d11	70879	52049 qy39f07	98233 q155d12	55096 wi48b08	17709 wk25c11	496105 HS_5075	53262 qy56f03.	54684 wq34h12.	33790 tt28e10.	85362 wl92h04.	38416 tt31g03.	06218 wz93g05.	31047 hh91d11.	85532 zn44ell.	09181 oll2b04.	14567 EST18646	57137 nl74b05.	39792 ws27c06.	06771 wf15a09.	36333 qd30a08.	28497 ds02h12.	03110 ok52b03.	//393 nru/106.	SOUTH ATTROOP.	40000 OQ49600.	091/3 WISUCU4.	37358 th98f09	AI818660 wk89c11.x	55664 zl75f06.	99733 tm91q12.	98040 wh80q12.	59901 xj34d12.	7552 wp78f11.	01012 tg91f04.	79957 tm73d10.	45973 qk45d10.	55075 wy99c10.	56826 tt54c09.	I221498 qg87a12.	703354 wd93c0	1057178 oy78b02.
SUMMARIES	OI .	AI39460	AW32849	AI87138	AI87087	AI36204	AI19823	AI76509	AI817709	3 AQ4961	AI36326	AI95468	AI63379	AI88536	AI63841	AW00621	AW63104	AA08553	AA90918	AA31456	AA55713	AI98979	AI80677	AI18633	AW32849	AA90311	AA8 / 29	AWLYC45	AA94000	AIBOUL	A1091/2	AI818660	AA05566	AI49973	AI79804	AW16990	AI93755	AI40101	AI47995	AI24597	AW05507	AI65682	AI22149	AI70335	AI05717
	Length DB	566 3	48 7	90 4	79 4	80 3	79 3	74 4	29 4	14 1	08	63 4	31 4	28 4	28 4	9 6/	80 7	46 2	26 3	00	99 2	16 4	31 4	05	96 7	φ. 	200	4.0	7 7 7 7 7 7	200	9 e	465 44	41 2	88 4	06 4	33 6	19 4	10 3	21 4	50 3	39 6	57 .4	37 3	97 .4	22.3
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ALIGNMENTS

RESULT 1 A1394605 C 566 bp mRNA EST 30-MAR-1999 LOCUS A1394505.x1 NCI_CGAP_CLL1 HOMO SAPIENS CDNA CLONE IMAGE:2108696 3' SERINITION tg13905.x1 NCI_CGAP_CLL1 HOMO SAPIENS CDNA CLONE IMAGE:2108696 3' SIMilar to SW:CDN2_HUMAN P42771 CYCLIN-DEPENDENT KINASE 4 INHIBITOR

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CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

Www-bio.lini.gov/bbrp//mage/image.html

Insert Length: 845 Std Error: 0.00

Seq primer: 40UP from Gibco

High quality sequence stop: 444.
                                                                                                                                                                 AIB71381 590 bp mRNA EST 07-MAR-2000 w181d11.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2431317 3' similar to TR:Q16361 Q16361 CELL CYCLE NEGATIVE REGULATOR BETA FORM 7, mRNA sequence.

AIB71381. GI:5545430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: Robert_Strausberg@nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chordata; Craniata; Vertebrata; Euteleostomí;
Primates; Catarrhini; Hominidae; Homo.
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1 (bases; Ditheria; Primates; Catarrhini; Hominidae; Homo.

NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index Unpublished (1998)

On Oct 30, 1998 this sequence version replaced gi:3813427.

Tel: (301) 496-1550

Email: Robert_Strausberg@nih.gov
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/clone=lib="NCI_CGAP_Brn25"
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/lab_host="DH10B"
242; Conservative
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NIH-WGC http://www.ncbi.nlm.nih.gov/MGC/.

National Institutes of Health, Mammalian Gene Collection (MGC)

On Apr 7, 1998 this sequence version replaced g1:3036295.

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert Strausbergenih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Edge BioSystems

CDNA Library Preparation: Edge BioSystems

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLML)

DNA Sequencing by: NIH Intramural Sequencing Center (NISC)

Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LIML at:

Www-bio.llnl.gov/bary/image/.image.html

Plate: LCM0030 row: O column: 24

Seq primer: -21M13 forward primer (ABI).
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1. 648

/organism="Homo saplens"
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/clone="IMAGE:2847599"
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                                                     AW328496 648 bp mRNA EST 28-JAN-2000 ds02h12.x1 NIH_MGC_4 Homo sapiens cDNA clone IMAGE:2847599 5', mRNA
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JOURNAL

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FEATURES

ACCESSION VERSION KEYWORDS SOURCE

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CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing Dy: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.lnl.gov/bbrp/image/timage.html Insert Length: 884 Std Error: 0.00 Seq primer: -40UP from Glbco High quality sequence stop: 321.
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Tel: (301) 496-1550
Email: Robert Strausberg@nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
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1 (bases 1 to 580)
NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index Unpublished (1998)
  CTGGGGTCGTCTGCCCGTGGACTTGGCCGAGGGGGGGCCACGCGCGACGTTGCAGGGTA 716
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information can be
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NCIXINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index Unpublished (1998)

On May 18, 1998 this sequence version replaced gi:3136859.

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert_Strausberg@nih.gov
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                                                                                         657 CTGGGGTCGTCTGCCCGTGGACTTGGCCGAGGAGCGGGGCCACCGCGACGTTGCAGGGTA 716
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Bonaldo, Ph.D.
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Pred. No. 1.4e-42;
0; Mismatches 22; Indels 0;
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Insert Length: 819 Std Error: 0.00
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High quality sequence stop: 474.
Location/Qualifiers
                                                                                                                                                   717 CCTGCGCACAGCCACGGGGGAC 738
                                                                                                                                                                           CCTGCGCGCGCTGCGGGGGGC 306
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/clone="IMAGE:2393463"
/clone_lib="NCI_CGAP_Co16"
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/db_xref="taxon:9606"
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                                                                                                                            Query Match 26.8%;
Best Local Similarity 91.2%;
Matches 238; Conservative
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                                                          113
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LOCUS
DEFINITION
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SOURCE
ORGANISM
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                                                        BASE COUNT
ORIGIN
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VERSION
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AUTHORS
TITLE
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www-bio.llnl.gov/bbrp/lmage/image.html
Insert Length: 729 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AI198233 579 bp mRNA EST 02-DEC-1998 q155d12.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:1860407 3' similar to TR:016361 016361 CELL CYCLE NEGATIVE REGULATOR BETA FORM ; contains LTR9.b3 TAR1 TAR1 repetitive element; , mRNA sequence.

AI198233.1 GI:3750839
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(Dases 1 to 579)
NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NAIJONAL Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BRGAP), Tumor Gene Index
Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.
                                                                                                                                                                                                                  959
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                                                                                                         557 CCAGGICAIGAIGAIGGGCAGCGCICGAGIGGCGGAGCIGCIGCIGCICCACCGCGCGGGAA 498
                                                                                                                                            GCCCAACTGCGCAGACCCTGCCACTCTCACCCGACCGGTGCATGATGCTGCCCGGGAGGG 596
                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
                                                                         CCAGGTCATGATGATGGCCAGCGCCCGCGTGGCGGAGCTGCTGCTGCTCCACGGCGCGGA
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   DB 38; Length 580;
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/db_xref="taxon:9606"
/clone="InAGE:1860407"
/clone_lib="NCI_CGAP_Brn25"
/lssue_type="anaplastic oligodendroglioma"
/lab_host="DH108"
                                      Indels
                                    23;
   Score 225.2; DB 3
Pred. No. 3.3e-42;
0; Mismatches 23
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High quality sequence stop: 459.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                       CCTGCGCACAGCCACGGGGGAC 738
                                                                                                                                                                                                                                                                                                                                                                                        317 cerecececececeses 296
Query Match 26.9%;
Best Local Similarity 91.2%;
Matches 239; Conservative (
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VERSION
KEYWORDS
SOURCE
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TITLE
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Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck, M.D., Ph.D.

CDNA Library Paragration: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution. NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 854 Std Error: 0.00
Seq primer: 40UP from Gibco
High quality sequence stops: 400.
T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized, and was constructed by Bento Soares and M-Estima Bonaldo." I others.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AI765096 774 bp mRNA EST 21-DEC-1999 wi48b08.x1 NCI_CGAP_CO16 Homo sapiens cDNA clone IMAGE:2393463 3/ similar to TR:Q13399 Q13399 HYPOTHETICAL 18.1 KDA PROTEIN ; contains LTR9.b3 MER22 repetitive element ;, mRNA sequence.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

(Dases 1 to 774)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

On Feb 22, 1999 this sequence version replaced gi:4283180.

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert_Strausberg@hih.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  658 TGGGGTCGTCTGCCCGTGGACTTGGCCGAGGGGGGGCCACCGCGCGACGTTGCAGGTAC 717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              657
                                                                                                                                                                                                                                                                                                                                                                                                           478 CAGGTCATGATGATGGGCCAGCGCCGGGGGGGGGGGCTGCTGCTGCTCCACGGCGGGGG 537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        555 CAGGTCATGATGATGGCCAGCGCCCGAGTGGCGAAGCTGCTGCTGCTCCACAGCGCGAAG 496
                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      538 CCCAACTGCGCAGACCCTGCCACTCTCACCCGACCGGTGCATGATGCTGCCCGGGAGGGC
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Pred. No. 5.6e-42;
0; Mismatches 23; Indels 0;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 614)
Mahalras,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Mahara,, Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
Hood,L.
Clone distribution: NCI-CGAP clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             648 GCGCGATGCCTGGGGTCGTCTGCCCGTGGACTTGGCCGAGGAGGGGGGCCACCGCGACGT 707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            624 GCNGCTGTGGCCCTCGTGCTGATGCTACTGAGAGCCCAGCGTCTAGGGCAGCAGCAGCGCTT 565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  528 CGCCCCGGAGCCCAACTGCGCAGACCCTGCCACTCTCACCCGACCGGTGCATGATGCTGC 587
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                408 GAAGGTGCGACACTCCTGGGAAGCCGGCGCGGATCCCAACGGAGTCAACCGTTTCGGGAG 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AQ496105 614 bp DNA GSS 28-APR-1999 HS_5075_A1_F12_T7 RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=651 Col=23 ROW=K, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  564 CCTAGAAGACCAGGTCATGATGATGAT-GGCAGCGCCGAAGTGGCGGAGCTGCTGCTGCTCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 219.4; DB 44; Length 729;
Pred. No. 7.2e-41;
0; Mismatches 63; Indels 1;
                                                                                                                                                                                                          /db_xref="taxon:9606"
/clone="INAGE:2413364"
/clone_lib="NCI_CGAP_Brn25"
/tissue_type="anaplastic oligodendroglioma"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 others
                 found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/lmage/lmage.html
Insert Length: 848 Std Error: 0.00
Seq primer: -400pf from Gibco
High quality sequence stop: 468.
Location/Qualifiers
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                                                                                                                                                                                       /organism-"Homo sapiens"
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Best Local Similarity 80.7%;
Matches 267; Conservative
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                                                                                                                                                                   source
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AUTHORS
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 729)
S NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Canner institute / National Institute of Neurological
Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/BTGAP), Tumor Gene Index
U Onpublished (1998)
On Apr 7, 1998 this sequence version replaced gi:3035534.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@uih.gov.
Email: Robert_Strausberg@uih.gov.
                                         /note-"Organ: colon; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA from the normalized library NCI_CGAP_CO10 was prepared, and so circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs (rom a pool of 5,000 clones made from the same library (cloneIDS 1057416-106125, and 1144584-14535)).
Subtraction by Bento Soares and M. Fatima Bonaldo. " 220 c 221 g 179 t lothers
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DNA Sequencing by: Washington University Genome Sequencing Center
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           531
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          656 GTGGGCCATCGTGCTTATGCTATTGAGGAGCCCAGCGTTTAGGGCAGCAGCGCTTCCTA 597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   591
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                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  712 GGGTACCTGCGCACAGCCACGGGGGACTGACGCCAGGTTCCCCAGCCGCCCACAA 766
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                                                                                                                                                                                                                                                                                                                                                      DB 44; Length 774;
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                                                                                                                                                                                                                                                                                                                                                   Score 223.8; DB 44; Length
Pred. No. 7.1e-42;
0; Mismatches 82; Indels
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/tissue_type="colon
                      /lab_host="DH10B"
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AI817709.1 GI:5436788
                                                                                                                                                                                                                                                                                                                                                   26.7%;
76.9%;
                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 76.9
Matches 273; Conservative
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AI817709/C
LOCUS
DEFINITION
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CONA Library Arrayed by: Greg Lennon, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

CDNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCT-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

WWW-blo.llni.gov/Dbrp/Inage/Aimage.html

Insert Length: 872 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 394.
   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Bases 1 to 708)
NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
Distorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index
Onpublished (1998)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                411 GGIGCGACACTCCTGGGAAGCCGGCGGGATCCCAACGGAGTCAACCGTTTCGGGAGGCG 470
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    607 GCTGTGGCCTTCGTGCTGATGCTGAGAAGCCAGCGTCTAGGGCAGCAGCGCGCTTCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CGATGCCTGGGGTCTCTGCCCGTGGACTTGGCCGAGGAGCGGGGCCACCGCGACGTTGC
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                                                                                                                                                                                                                                                                                                                                                                         Email: Robert_Strausberg@nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
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                                                                                                                            On Dec 15, 1999 this sequence version replaced gi:4575297.
Contect: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Mashington
University of Mashington
University of Mashington
University of Mashington.
University Radio Geoup Mashington.
University Resources (Hitp://Pacpac.med.buffalo.edu/ordering_bac.htm)
Or from Resear h Genetics (Info@fresgen.com). BAC end Web Server:
University Mashington.edu
Plate: 651 row: K column: 23
Seq primer: T7
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
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/clone="late=651 Col=23 Row=K"
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/sex="male"
/note="vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
/note="vector: pBACe3.6; Site_1 = CoRI; Site_1 = CoRI; Site_2 = Size_2 = Siz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             478 CAGGTCATGATGATGGCAGCGCCGCGTGGCGGAGCTGCTGCTGCTCCTCCACGGCGCGGGAG 537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      538 CCCAACTGCGCAGACCCTGCCACTCTCACCCGACCGGTGCATGATGCTGCCCGGGAGGGC 597
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Sequence-tagged connectors: A sequence approach to mapping scanning the human genome Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999) 99380589
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 26.2%; Score 219.2; DB 103; Lengt
Best Local Similarity 85.1%; Pred. No. 7.9e-41;
Matches 245; Conservative 0; Mismatches 43; Indels
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Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550
Email: Robert-Strausberg and the contact: Robert Strausberg and the contact: Robert Strausberg and the contact: Robert Strausberg and the contact and contact and the contact and contact a
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144 c 163 g 116 t lothers
                                                                                                                                                                                                                                                                                               A1633790 531 bp mRNA EST 14-DEC-1999 tt288el.0x1 NCI_GCAB-GC6 Homo sapiens CDNA clone IMAGE:2242122 3's similar to TR:016361 Q16361 CELL CYCLE NEGATIVE REGULAROR BETA FORM ; contains LTR9.b3 TAR1 repetitive element ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 531)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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370 GGGCCGTCTGCCCGTGGACCTGGCTGAGGAGCTGGGCCATCGCGATGTCGCACGGTACCT 311
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Pred. No. 1.1e-37;
0; Mismatches 20; Indels 0;
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/lab_host="DH10B"
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/db_xref="taxon:9606"
/clone="IMAGE:2242122"
/clone_lib="NCI_CGAP_GC6"
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                                                                 720 GCGCACAGCCACGGGGGAC 738
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Best Local Similarity 91.6%;
Matches 217; Conservative
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Unpublished (1997)
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DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
Glound through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 613 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stops: 460.

Location/Qualifiers
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                                                                                            A1954684 563 bp mRNA EST 08-MAR-2000 wq34h12.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2473223 3' similar to SW:CDN2_HUMAN P42771 CYCLIN-DEPENDENT KINASE 4 INHIBITOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@hih.gov
Email: Robert_Strausberg@hih.gov
R. Emmert-Buck, M.D., Ph.D., Michael
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            540 CAACTGCGCAGACCCTGCCACTCTCACCCGACCGGTGCATGATGCTGCCCGGGAGGGCTT 599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGGTCGTCTCCCCGTGGACTTGGCCGAGGAGCGGGCCACCGCGACGTTGCAGGTACCT 719
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCTGGACACGCTGGTGGTGCTGCACCGGGCCGGGGCGCGGCTGGACGTGCGCACGATGCCTG 659
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Pred. No. 1.7e-39;
0; Mismatches 21; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="IMAGE:2473223"
/clone_lib="NCI_CGAP_GC6"
/tissue_type="pooled germ cell tumors"
/lab_host="DH108"
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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ilarity 91.5%;
Conservative
                                                                                                                                                                                                   mRNA sequence.
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A1954684
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Matches 237
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Sequencing Center information can be

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AI638416 528 bp mRNA EST 14-DEC-1999 tt31g03.x1 NCI_CGAP_GC6 Homo sapiens CDNA clone IMAGE:2242420 3' similar to TR:Q16361 Q16361 CELL CYCLE NEGATIVE REGULATOR BETA FORM AI638416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
Clond through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 648 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 462.
Location/Qualiflers
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143 c 163 g 114 t 2 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tumor Gene Index
Unpublished (1997)
On Apr 7, 1998 this sequence version replaced g1:3036438.
Contact: Robert Strausberg, Ph.D.
Enel: (301) 496-1550
Email: Robert_Strausbergenth.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 528) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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625 CGGCCGGGGCGCGCGCTGGACGTGCGCGATGCCTGGGGTCGTCTGCCCGTGGACTTGGCC
                                                                                                                        685 GAGGAGCGGGCCACCGCGACGTTGCAGGGTACCTGCGCACAGCCACGGGGGAC 738
                                                                                                                                                                                                          24.4%; Score 204.6; DB 42; Length 528; 91.1%; Pred. No. 1.8e-37; Live 0; Mismatches 21; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="pooled_germ cell tumors" /lab_host="DH10B"
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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/clone_lib="NCI_CGAP_GC
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Matches 216; Conservative
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DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llol.gov/Dbrp/Image/image.html
Insart Length: 626 Std Error: 0.00
Seq primer: -400P from Gibco
                                                                                                                                                                                                                                                                           AI885362 528 bp mRNA EST 07-MAR-2000 w192h04.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2432407 3' similar to SW:CDN2_HUMAN P42771 CYCLIN-DEPENDENT KINASE 4 INHIBITOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi; Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi; Mammalia: Eutheria: Primates: Catarrhini; Hominidae: Homo.

1 (bases 1 to 528)

NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BFGAP). Tumor Gene Index

Unpublished (1998)

Contact: Robert Strausberg, Ph.D.
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                       565 ACCCGACCGGTGCATGATGCTGCCCGGGAGGCCTTCCTGGACACGCTGGTGGTGGTGCTGCAC 624
CACCGGCCCGGGCGCGCTGGACGTGCGGATGCCTGGGGTCGTCTGCCCGTGGACTTG 681
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Bonaldo, Ph.D.
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Location/Qualifiers
1. .528
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AI885362
AI885362.1 GI:5590526
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                                                                                                                                                                                                                                                                              AW006218 579 bp mRNA EST 10-SEP-1999 wz93905.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2566424 3' similar to TR:Q16361 Q16361 CELL CYCLE NEGATIVE REGULATOR BETA FORM 3', mRNA sequence.
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Eukaryofta...

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 579)

NCI/NINDS-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NCI/NINDS-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/PRTGAP), Tumor Gene Index Unpublished (1998)

On Oct 6, 1998 this sequence version replaced gi:3705694.

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: Robert_Strausberg@nih.gov
Ilssue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
                                                 621
                                                                                                                                          CACCGGGCCGGCGCGCTGGACGTGCGCGATGCCTGGGGGCCGTCTGCCCGTGGACCTG 349
528 CGAGTGGCGGAGCTGCTGCTCCACGGCGCGGAGCCCAACTGCGNCGACNCCGCCACT 469
                                                                                                        CACCGGGCCGGGGCGCGCTGGACGTGCGCGATGCCTGGGGTCGTCTGCCCGTGGACTTG 681
                                                                                                                                                                                               682 GCCGAGGAGCGGGGCCACCGCGACGTTGCAGGGTACCTGCGCACAGCCACGGGGGGAC 738
                                 562 CTCACCCGACCGGTGCATGATGCTGCCCGGGAGGCTTCCTGGACACGCTGGTGGTGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 579;
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Pred. No. 2.8e-37;
0; Mismatches 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
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Best Local Similarity 90.2
Matches 239; Conservative
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Search completed: July 21, 2000, 02:48:45 Job time: 9640 sec

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| L36844 Homo sapiens (clone p151 | U17075 Human p14-CDK inhibitor | U17075 Human p14-CDK inhibitor | U17075 Human p14-CDK inhibitor | AR001326 Sequence 15 from paten | AR001326 Sequence 15 from paten | I41160 Sequence 15 from paten | I41160 Sequence 15 from paten | AF004819 Homo sapiens alternati | S79760 Ink4 | Tats, kidney, mRNA | AR002815 Sequence 1 from paten | AR001314 Sequence 1 from patent | AR001314 Sequence 1 from patent | AR001314 Sequence 36 from patent | AR001316 Sequence 36 from patent | AR001316 Sequence 36 from patent | AR001317 Sequence 5 from patent | AR013698 Felis catus gene for | S7835 tumor suppressor gene, | S7835 tumor gene gene gene, | S7835 tumor gene gene, | S7835 tumor gene gene, | S7835 tumor gene, | S7835 tumor gene, | S7835 
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                                                                                                                         About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
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Hannon,G.J. and Beach,D.
p151NK4B is a potential effector of TGF-beta induced cell cycle
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DEFINITION Homo sapiens (clone p151NK4B/HA5) CDK inhibitory protein mRNA,
complete cds.
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        1.2e-22
5.6e-24
4.2e-24
3.8e-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /cell_type="keratinocyte"
/clone="pl5INK4B/HA5"
11. 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1. .837
/organism="Homo saplens"
/db_xref="taxon:9606"
/cell_line="HaCaT"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         L36844 G1:556197
L36844 I G1:556197
CDK inhibitory protein.
Homo sapiens CDNA to mRNA.
Homo sapiens
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        551.95
575.88
578.04
578.89
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94359613
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49

83

us-09-016-869a-4.rge

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422 IGGAAGCCGGCGCGCATCCCAACGGAGTCAACCGTTTCGGGAGGCGCGCG 471
                                                                                                                                                                                                                                                                     100 ArgAlaGlyAlaArgLeuAspValArgAspAlaTrpGlyArgLeuProVa 116
                                                                                                                                                                                                                                                                                                                                                                                                                 572 recardarcereceesasseerrecessacaceersersersers 621
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                                                                                                                                                                                                                                                                                                                       83 alHisAspAlaAlaArgGluGlyPheLeuAspThrLeuValValLeuHis 99
                                 17 yleualathr...ProalaargGlyLeuValGluLysValargHisSerT
||||||||::
||TGGCCAGCGCGGGGGGGACTAGTGGAGAAGGTGCGACAGCTCC
                                                                                                       33 rpGluAlaGlyAlaAspProAsnGlyValAsnArgPheGlyArgArgAla
 322 ATGCGCGAGGAGAACAAGGGCATGCCCAGTGGGGGGGGGCGCAGCGATGAGGG
                                                                                                                                                                                                                                                    uHisGlyAlaGluProAsnCysAlaAspProAlaThrLeuThrArgProV
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Identity: 95.652
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Patent: US 5739027-A 15 14-APR-1998;
Location/Qualifiers
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225 c 292 g
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1 (bases 1 to 751)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         722 CAGCCACGGGGGAC 735
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Locus AR001326
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VERSION
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="p14-CDK inhibitor"
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/protein_id="aac50075.1"
/db_xref="G1:639716"
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RFGRRAIQVMMGSARVAELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRA
RFGRRAIQVMMGLAPVDLAEERHRDVAGYLRHATGD"
1 223 c. 286 g 102 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 738)
Guan, K.L., Jenkins, C.W., Li, Y., Nichols, M.A., Wu, X., O'Keefe, C.L., Mattera, A.G. and Xiongy Y.
Agrera, A.G. and Xiongy Y.
Growth suppression by pil8, a p161NK4/MTS1- and
p14INK4B/MTS2-related CDK6 inhibitor, correlates with wild-type pRb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (09-NOV-1994) Kun-Liang Guan, Biological Chemistry,
University of Michigan, 1301 East Catherine, Ann Arbor, MI 48109,
USA
                                                                                                                                                                                                                                                                                                                                                                                             27-JAN-1995
                                                   pLeuAlaGluGluArgGlyHisArgAspValAlaGlyTyrLeuArgThrA 134
                                                                                                                                                                                                                 1 MetargGluGluAsnLysGlyMetProSerGlyGlyGlyGlySerAspGluGl 17
                    528 CGGCGCGGAGCCCAACTGCGCAGACCCTGCCACTCTCACCCGACCGGTGC
HSU17075 738 bp mRNA PRI Human p14-CDK inhibitor mRNA, complete cds. U17075 U17075.1 GI:639715
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Percent Identity: 95.652
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/organism="Homo sapiens"
/db_xref="taxon:9606"
322. .738
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4.981
97.101
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US-09-016-869A-4 x HSU17075
                                                                                                                                                                                                                                                                                                                                         seq_name: gb_pr3:HSU17075
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LOCUS HSU17075
                                                                                                                                                                                                                                                                                                      728 CCACGGGGGAC 738
                                                                                                                                                                                                                                                                   134 laThrGlyAsp 137
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Percent Similarity:
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source

FEATURES

CDS

MEDLINE REFERENCE

JOURNAL

TITLE JOURNAL AUTHORS

BASE COUNT

KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

TITLE

DEFINITION

VERSION

628 117

101

04-DEC-1998

83

684

us-09-016-869a-4.rge

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100 ArgAlaGlyAlaArgLeuAspValArgAspAlaTrpGlyArgLeuProVa 116
385 TCTGGCCAGCGCCGCGCGCGGGACTAGTGGAGAAGGTGCGACAGCTCC 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17 yLeuAlaThr...ProAlaArgGlyLeuValGluLySValArgHisSerT 33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50 IleGlnValMetMetGlySerAlaArgValAlaGluLeuLeuLe 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              485 ATCCAGGTCATGATGATGGCCACCCCCCCGCGTGCCGGAGCTGCTGCT
                                                                                                           83 alHisAspAlaAlaArgGluGlyPheLeuAspThrLeuValValLeuHis
                                                    66 uHisGlyAlaGluProAsnCysAlaAspProAlaThrLeuThrArgProV
                                                                      535 CCACGGCGCGGAGCCCAACTGCGCAGACCCTGCCACTCTCACCCGACCGG
                                                                                                                                                                                           635 cegeccegeccegecreeacerececarecerecerecerere
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Percent Identity: 95.652
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M Unknown.
Unclassified.
Unclassified.
E 1 (bases 1 to 751)
S Stone,S., Jiang,P. and Kamb,A.
Mouse MrSI gener.
AL Patent: US 5843756-A 15 01-DEC-1998;
Location/Qualifiers
751 "...known" 104 t
                                                                                                                                                                                                                                                                                                                                                                                       5843756.
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AR062786
AR062786.1 GI:5990477
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4.981
97.101
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US-09-016-869A-4 x AR062786
                                                                                                                                                                                                                                                                                                     735 CAGCCACGGGGGAC 748
                                                                                                                                                                                                                                                                          133 hralaThrGlyAsp 137
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LOCUS AR062786
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JOURNAL
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Kamb. A.

Probes for MTS1 gene and polynucleotides encoding mutant MTS1 genes

Patent: US 5801236-A 15 01-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                              29-SEP-1999
                                                                                                                                                                                                                                                                                       635 CGGCCGGGCGCGCGCTGGACGTGCCGTGGGCTCGCCCCGT 684
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Percent Identity: 95.652
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US 5801236.
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1. .751
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225 c 292 g
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4.981
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Locus AR037506
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DEFINITION

VERSION KEYWORDS SOURCE ORGANISM

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FEATURES

BASE COUNT ORIGIN

REFERENCE AUTHORS TITLE JOURNAL

alignment_block

29-SEP-1999

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33 rpGluAlaGlyAlaAspProAsnGlyValAsnArgPheGlyArgArgAla 49
585 IGCAIGAIGCIGCCCGGGAGGGCIICCIGGACACGCIGGIGGIGCIGCAC
                                                                                                                                                                                                                                                                                                                AF004819.1 GI:2257934
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US-09-016-869A-4 x AF004819
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                                                                                                                                                133 hrAlaThrGlyAsp 137
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Locus AF004819
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Percent Similarity:
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                                                                                                                                                             100 ArgAlaGlyAlaArgLeuAspValArgAspAlaTrpGlyArgLeuProVa 116
                                                                                                                      335 ATGCGCGAGGAGAACAAGGGCATGCCCAGTGGGGGGGCGCAGCGATGAGGG 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         385 rerescensescessessessesses 434
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MetArgGluGluAsnLysGlyMetProSerGlyGlyGlyGlySerAspGluGl 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             yLeualaThr...ProalaargGlyLeuValGluLysValArgHisSerT 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33 rpGluAlaGlyAlaAspProAsnGlyValAsnArgPheGlyArgArgAla 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50 IleGlnValMetMetMetGlySerAlaArgValAlaGluLeuLeuLeuLe 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66 uHisGlyAlaGluProAsnCysAlaAspProAlaThrLeuThrArgProV 83
                                           83 alHisAspAlaAlaArgGluGlyPheLeuAspThrLeuValValLeuHis
                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 751)
Skolnick, M.H., Cannon-Albright, L.A. and Kamb, A. Germline mutations in the MTS gene
Patent: US 5624819-A 15 29-APR-1997;
                                                                                                                                                                                                                                                                                                                                PAT
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Percent Identity: 95.652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
                                                                                                                                                                                                                                                                                                                                         Sequence 15 from patent US 5624819. 141160. 151:2081750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to: 141160 from: 1 to: 751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="unknown"
225 c 292 a
                                                                                                                                                                                                                                                                                                                              751 bp
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4.981
97.101
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                                                                                                                                                                                                                         133 hrAlaThrGlyAsp 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Unclassified.
                                                                                                                                                                                                                                                                                                                seq_documentation_block:
LOCUS I41160
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Ratio:
Percent Similarity:
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Unknown.
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source

BASE COUNT

ORIGIN

JOURNAL FEATURES

TITLE

DEFINITION ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

REFERENCE AUTHORS alignment_block

17

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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Mammalia,
Eukaryota, Metazoa, Catarrhini, Hominidae, Homo.
I (bases I to 859)
I Sharian, Tilhonen, E. and Laiho, M.
Cloning and characterization of pl0, an alternatively spliced form of pl5 cyclin-dependent Kinase inhibitor
Cancer Res. 57 (14), 2966-2973 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (20-MAY-1997) Department of Virology, Haartman Institute,
University of Helsinki, P.O. Box 21, Helsinki 00014, Finland
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens alternative spliced form of p15 CDK inhibitor mRNA, complete cds.

AF004819
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634
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Gaps: 2
Percent Identity: 73.743
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Tsubari,M., Tithonen,E. and Laiho,M.
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                   ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukaryota; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

E 1 (basea 1 to 706.

I (basea 1 to 706.

Hino, O., Kobayashi, E., Hirayama, Y., Kobayashi, T., Kubo, Y.,

Tsuchiya, H., Kikuchi, Y. and Mitani, H.

Molecular genetic basis of renal carcinogenesis in the Eker rat
model of tuberous sclerosis (Tsc2)

Mol. Carcinog. 14 (1), 23-27 (1995)

E 96001392

Mol. Carcinog. 14 (1), 23-27 (1995)

GenBank staff at the National Library of Medicine created this entry (NCBI gibbsq 171930) from the original journal article.

This sequence comes from Fig. 1A.

Map location: 54

Location/Qualifiers

I. 706

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                                                                                                                                                                                                                                                                                                  108
                                                                                                                                                                                                                                     120 TGGAAGCCGCGCGGATCCCAACGGAGTCAACCGTTTCGGGAGGCGCGCG 469
                                                                                                                                                                                                                                                                                                                                                                                      28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note-"This sequence comes from Fig. la"
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                                                                                                                                                                                                                                                                                                                                                                   92 euAspThrLeuValValLeuHisArgAlaGlyAlaArgLeuAspValArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 125 gAspValAlaGlyTyrLeuArgThrAlaThrGlyAsp 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AWGRLPVDLAEEQGHRDIARYLHAATGD'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  s/9760 706 bp mRNA
Ink4 [rats, kidney, mRNA, 706 nt].
S/9760
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161. .553
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Rattus sp.
                                            50 IleGln....
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LOCUS S79760
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Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1301)
Quelle, D.E., Ashmun, R.A., Hannon, G.J., Rehberger, P.A., Trono, D., Richter, K.H., Walker, C., Beach, D., Sherr, C.J. and Serrano, M. Cloning and characterization of murine pl6INK4a and pl5INK4b genes oncogene 11 (4), 635-645 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 (bases 1 to 1301)
Quelle,D.E., Ashmun,R.A., Hannon,G.J., Rehberger,P.A., Trono,D.,
Richter,K.H., Walker,C., Beach,D., Sherr,C.J. and Serrano,M.
Direct Submission
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(Cdkn2b) mRNA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         143 CGGACCGGGGACAAGGCCATG...TTGGCCGCCGCCGCAGTGACGCGGGCCT 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                240 AAGCCGGCGCAGATCCCAACGCCGTCAACCGCTTCGGGAGGCGCCCGATC 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          290 CAGGICATGAIGAIGGCCAGCCCCAGGIGGCAGAGCIGIIGCICCICCA 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pLeuAlaGluGluArgGlyHisArgAspValAlaGlyTyrLeuArgThrA 134
                                                                                                                                                                                                                                                                                                                                                                                                18 uAlaThr ... ProAlaArgGlyLeuValGluLysValArgHisSerTrpG 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AF059567 1301 bp mRNA ROD MUS musculus cyclin dependent kinase inhibitor 2B
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                                                                                                                                                                                                                                                                                                             2 ArgGluGluAsnLysGlyMetProSerGlyGlyGlySerAspGluGlyLe
                                                                                                                                                                                                                                                                                                                                                                                                                                            190 GCCCACCGCCGCGCGCGGGACAGGTGGAGACGGTGCGGCAGCTCCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34 luAlaGlyAlaAspProAsnGlyValAsnArgPheGlyArgArgAlaile
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                                                                                                          Length: 137
Gaps: 2
Percent Identity: 82.482
121
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231
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                                                                                                        555.00
4.512
89.781
212
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US-09-016-869A-4 x S79760
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                                                                                                                                                      Percent Similarity:
                                                                                                                 Quality:
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us-09-016-869a-4.rge

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AR001314.1 GI:3963381
                                                                                                                                                                                                                                                                                                                                               545.50
4.623
92.188
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                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-016-869A-4 x AR062815
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                               seq_documentation_block:
LOCUS AR062815
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Ratio:
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                                                                                                                                                                                                                               FEATURES
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Submitted (14-APR-1998) Immunology and Oncology, National Center of Biotechnology, Campus de Cantoblanco, Madrid E-28049, Spain Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                333 ACCCAACTGGGCGGACCCTGCCACCTTACCAGACCTGTGCACGACGCAG 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CGGCTGGATGTGTGTGACGCCTGGGGCCGCCTGCCGGTAGACTTGGCTGA 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37 laAspProAsnGlyValAsnArgPheGlyArgArgAlaIleGlnValMet 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 AsnLysGlyMetProSerGlyGlyGlySerAspGluGlyLeuAlaThr.. 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21 .ProAlaArgGlyLeuValGluLysValArgHisSerTrpGluAlaGlyA 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MetMetGlySerAlaArgValAlaGluLeuLeuLeuLeuHisGlyAlaGl 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 70 uProAsnCysAlaAspProAlaThrLeuThrArgProValHisAspAlaA 87
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4.508
91.045
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US-09-016-869A-4 x AF059567
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Ratio:
Percent Similarity:
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                                              source
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   JOURNAL
                                                                                                                                                  gene
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29-SEP-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 spThrLeuValValLeuHisArgAlaGlyAlaArgLeuAspValArgAsp 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           110 AlaTrpGlyArgLeuProValAspLeuAlaGluGluArgGlyHisArgAs 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             107 ACCGCTTCGGGAGGCGCCCAATCCAGGTCATGATGATGGGCAGCGCCCAG 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11 GlyGlyGlySerAspGluGlyLeuAlaThr...ProAlaArgGlyLeuVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 GCCGCCAGTGACGCGGCCTGGCCACCGCGCGCGCGGGGGCAAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60 ValAlaGluLeuLeuLeuHisGlyAlaGluProAsnCysAlaAspPr
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                PAT
                                                                                                                                                                                                                                                                                                                                     Length: 128
Gaps: 1
Percent Identity: 85.156
                                                                                                                       Unclassified.

1 (bases 1 to 393)
Stone,S., Jang,P. and Kamb,A.
Mouse MTSI gene
Patent: US 5843756-A 45 01-DEC-1998;
ARU62815 393 bp DNA
Sequence 45 from patent US 5843756.
AR062815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pValAlaGlyTyrLeuArgThrAlaThrGlyAsp 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      from: 1 to: 393
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US 5739027
                                                                                                                                                                                                          Location/Qualifiers
1. .393
                                                                                                                                                                                                                                   /organism="unknown"
124 c 141 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_documentation_block:
LOCUS AR001314 471 bp
DEFINITION Sequence 1 from patent
                                                              AR062815.1 GI:5990506
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Percent Identity: 80.451
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            186
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            O
                                                                    506.50
4.404
86.466
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4.404
86.466
            153
                                                                                                                    alignment_block:
US-09-016-869A-4 x AR037494
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Locus AR062774
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Ratio:
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Percent Similarity:
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            68
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                                                          alignment_scores
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KEYWORDS
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ACCESSION
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TITLE
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Probes for MTS1 gene and polynucleotides encoding mutant MTS1 genes
Patent: US 5801236-A 1 01-SEP-1998;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                107 CGCTGCCCAACGCACATAGTTACGGTCGGAGGCCGATCCAGGTCATG 156
                                                                                                                                                                                                                                                                                                                                                                                                                                  ArgLeuAspvalArgAspAlaTrpGlyArgLeuProValAspLeuAlaG1 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37 laAspProAsnGlyValAsnArgPheGlyArgArgAlaIleGlnValMet 53
                                                                                                                                                                                                                                                                                     9 ProSerGlyGlyGlySerAspGlu........GlyLeuAlaThr.. 20
                                                                                                                                                                                                                                                                                                                                     21 .ProAlaArgGlyLeuValGluLysValArgHisSerTrpGluAlaGlyA 37
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                                                                                                                                                                                         Gaps: 2
Percent Identity: 80.451
/ Unknown.
Unclassified.
E 1 (bases 1 to 471)
S Kamb,A.
MTSIE1 beta gene
MTSIE1 beta gene
AL Patent: US 5739027-A 1 14-APR-1998;
Location/Qualifiers
. 471
"...known" 64
                                                                                                                                                                               Length:
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Sequence 1 from patent US 5801236.
AR037494
                                                                                                    /organism="unknown"
153 c 186 g
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Unclassified.
1 (bases 1 to 471)
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4.404
86.466
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US-09-016-869A-4 x AR001314
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LOCUS AR037494
                                                                                                                                                                             Quality:
Ratio:
Percent Similarity:
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AUTHORS
TITLE
JOURNAL
FEATURES
                                                       TITLE
JOURNAL
FEATURES
                                                                                                                   BASE COUNT
                                REFERENCE
AUTHORS
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29-SEP-1999
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                                                                                                                                                 21 .ProAlaArgGlyLeuValGluLysValArgHisSerTrpGluAlaGlyA 37
                                                                                                                                                                                                                                                  laAspProAsnGlyValAsnArgPheGlyArgArgAlaIleGlnValMet 53
                                                                                                                                                                                                                                                                                                                                                                    uProAsnCysAlaAspProAlaThrLeuThrArgProValHisAspAlaA 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120 uGluArgGlyHisArgAspValAlaGlyTyrLeuArgThrAlaThrGly 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 ProSerGlyGlyGlySerAspGlu.........GlyLeuAlaThr.. 20
Length: 133
Gaps: 2
Percent Identity: 80.451
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unclassified.

1 (bases 1 to 471)
Stone,S., Jang,P. and Kamb,A.
Mouse MISI gene
Patent: US 5843756-A 1 01-DEC-1998;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64
                                                                                                      to: 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1 from patent US 5843756.
AR062774
AR062774.1 GI:5990465
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153 c 186 g
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53

37

256

87

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57 CCCGCCCCGGGTCGGGTAGAGGAGGTGCGGGCGCTGCTGGAGGCGGGGG 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           107 CGCTGCCCAACGCACCGAATAGTTACGGTCGGAGGCCGATCCAGGTCATG 156
                                                                                                                                                                                                                                                                                                                                                                                                         9 ProSerGlyGlyGlyGlySerAspGlu.........GlyLeuAlaThr.. 20
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                                                                                                                                                                                                                                                                                                                                                                                        120 uGluArgGlyHisArgAspValAlaGlyTyrLeuArgThrAlaThrGly 136
                                                                                                                                                                                         21 .ProAlaArgGlyLeuValGluLysValArgHisSerTrpGluAlaGlyA
                                                            37 laAspProAsnGlyValAsnArgPheGlyArgArgAlaIleGlnValMet
                                                                                  21 .ProAlaArgGlyLeuValGluLysValArgHisSerTrpGluAlaGlyA
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Gaps: 2
Percent Identity: 80.451
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MTSIE1.beta. gene
Patent: US 5739027-A 36 14-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCUS AR001346 947 bp DNA
DEFINITION Sequence 36 from patent US 5739027.
ACCESSION AR001346
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271 c 274 q
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4.404
86.466
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US-09-016-869A-4 x AR001346
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Ratio:
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VERSION
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TITLE
JOURNAL
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SOURCE
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                                                                                                                                                                                                        87 laArgGluGlyPheLeuAspThrLeuValValLeuHisArgAlaGlyAla 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    104 ArgLeuAspValArgAspAlaTrpGlyArgLeuProValAspLeuAlaG1 120
                                                                                                                                                              257 cccescagescriccresacacecresacerecrecacceseces
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                                                                               and Kamb, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PAT
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Percent Identity: 80.451
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Unknown.

Unclassified.

1 (bases 1 to 471)

S kolnick,M.H., Cannon-Albright,L.A. angermilne mutations in the MTS gene Germilne mutations in the MTS gene AL Patent: US 5624819-A 1 29-APR-1997;

Location/Qualifiers
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    141148
    471 bp
    DNA

    26quence 1 from patent US 5624819.

    141148

    141148.1 GI:2081738

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a 153 c 186 g
                                               from: 1
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                                                                               9 ProSerGlyGlyGlySerAspGlu.
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Ratio: 4.404
nilarity: 86.466
                                             Align seg 1/1 to: AR062774
             US-09-016-869A-4 x AR062774
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US-09-016-869A-4 x I41148
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LOCUS I41148
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alignment_block
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source

FEATURES

BASE COUNT

ORIGIN

TITLE

AUTHORS REFERENCE

SOURCE

DEFINITION ACCESSION VERSION KEYWORDS

04-DEC-1998

PAT

26 37

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157 ATGATGGGCAGCCCCAGTGGCGGAGCTGCTGCTCCTCCACGCGCGGA 206
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70 uProAsnCysAlaAspProAlaThrLeuThrArgProValHisAspAlaA 87		1
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4.981
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US-09-016-869A-4 x T00745
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Ratio: ,
N_Geneseq_36:V70586
N_Geneseq_36:T00744
N_Geneseq_36:Q99164
N_Geneseq_36:T69780
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Multiple tumour suppressor 2 (N Human multiple tumour suppressor inturated party protein multiple tumour suppressor Truncated p27/p16 fusion protein Human multiple tumour suppressor CDNA encoding a human multiple tumour suppressor I munour suppressor p16 coding sequence of the multiple CDNA encoding a human multiple tumour suppressor I munour suppressor p16 coding sequence of the multiple CDNA encoding a human multiple tumour suppressor I munan p1627 fusion protein Human p1663/p27 fusion protein Human multiple tumour suppressor I (N Cell-cycle regulatory protein Human multiple tumour suppressor I (N Cell-cycle regulatory protein Human multiple tumour suppressor I (N Human multiple sequence of the multiple sequence of the multiple multiple sequence of the multiple sequence of the multiple multiple seq
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Query length: 137
Database: N_Geneseq_36:*
Database sequences: 311585
Database length: 125096042
Search time (sec): 109.050000
                                                          Date: Jul 21, 2000 9:30 AM
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N_Geneseq_36:063491
N_Geneseq_36:T00749
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Sequence
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Human multiple tumour suppr
Multiple tumour suppressor
Human MTS polypeptide, MTS1
Human multiple tumour suppr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Detecting polymorphism associated with cancer pre:disposition - also DNA, vectors and host cells e.g. for gene or protein replacement therapy and drug screening is e.g. for gene or protein replacement blischosure; Pages 102-103; 148pp; English.

An individual can be diagnosed as having a predisposition to cancer by detecting an alteration in the wild type multiple tumour suppressor (MTS) gene, using gene probes which hybridise to the MTS2 gene ORF T00745 (which encodes R81702). The above assay can also be used in the diagnosis and prognosis of malanoma, lymphoma, leukaemia and pancreas, breast and thyroid cancers, etc. .

25 C; 292 G; 104 T;
                                                                                                                                                                             seq_documentation_block:

ID T00745 standard; cDNA; 751 BP.

AC T00745; standard; cDNA; 751 BP.

DT 08-MAX-1996 (first entry)

BE Multiple tumour suppressor 2 (MTS2) gene ORF.

KW Multiple tumour suppressor 1 MTS2; cancer; diagnosis; assay; predisposition; melanoma; leukaemia; lymphoma; prognosis; KW pancreas; breast; thyroid; open reading frame; ORF; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  335 ATGCGCGAGGAGAACAAGGGCATGCCCAGTGGGGGGGGCGCAGCGATGAGGG 384
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Gaps: 1
Percent Identity: 95.652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PR 18-MAR-1994; US-214582.
PR 18-MAR-1994; US-215087.
PR 14-APR-1994; US-215086.
PR 10-JUN-1994; US-251369.
PR 01-JUN-1994; US-251369.
PR 01-JUN-1994; US-251938.
A (UTAH ) WINV UTAH RES FOUND.
I Cannon-Albright LA, Ramb A, Skolnick MH; P-PSDB; R952844.
P-PSDB; R97102.
Detecting 10-21468644.
8.5e-36
4.1e-33
4.1e-33
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779.14
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to: 751

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from: 1
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(UTAH ) UNIV UTAH RES FOUND
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18-MAR-1994; US-215086.
18-MAR-1994; US-227369.
14-APR-1994; US-227369.
01-JUN-1994; WO-U03537.
07-JUN-1995; US-474177.
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                            to: 099165
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                            Align seg 1/1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wild-type multiple tumour suppressor (MTS) gene and mutant sequences - useful in diagnosis, prognosis and therapy of human cancer, e.g. melanoma or leukaemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-MAY-1996 (first entry)

Human multiple tumour suppressor polypeptide, MTS2 encoding cDNA.

Multiple tumour suppressor; El-alpha; diagnosis; cancer; leukaemia; astrocytoma; glioblastoma; Hodgkin's lymphoma; melanoma; glioma; gene therapy; chronic; ds.

Homo sapiens.
                                                                                                                                                100 ArgalaGlyAlaArgLeuAspValArgAspAlaTrpGlyArgLeuProVa 116
                                                                                                                                                                                                                                               535 CCACGCCCCGAGCCCAACTGCGCAGACCCTGCCACTCTCACCCGACCGG 584
                                                                                              585 recargargereceeseaseerrecresacacsersersersers 634
                                                                                                                                                                                                  alHisAspAlaAlaArgGluGlyPheLeuAspThrLeuValValLeuHis 99
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Sequence 751 BP; 130 A; 225 C; 292 G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          335. .751
/*tag= a
/product= MTS2
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ID Q99165 standard; cDNA; 751 BP.
AC Q99165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-SEP-1995.
17-MAR-1995, UG3316.
18-MAR-1994; US-214581.
18-MAR-1994; US-214582.
18-MAR-1994; US-215086.
18-MAR-1994; US-215087.
14-APR-1994; US-217369.
01-UUN-1994; US-227369.
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97.101
                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name: N_Geneseq_36:Q99165
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                                                                                                                                                                                                                                                                                                                                                                                                       735 CAGCCACGGGGAC 748
                                                                                                                                                                                                                                                                                                                                                        133 hrAlaThrGlyAsp 137
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US-09-016-869A-4 x Q99165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kamb A;
WPI; 95-344401/44.
P-PSDB; R80948.
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N
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Human; multiple; tumour; suppressor; MTS2; cancer; diagnosis; ds
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WPI; 97-258217/23.

WPPI; 97-258217/23.

P-PRDB; W1925.

Human mutant multiple tumour suppressor gene sequences - for production of recombinant mutant polypeptide(s)

Disclosure; Columns 75-78; 72pp; English.

Disclosure; Columns 75-78; 72pp; English.

(MES), useful in cancer disagnossis.

(MES), useful in cancer disagnossis.

Sequence 751 Bp; 130 A; 225 C; 292 G; 104 T;
ArgalaGlyAlaArgLeuAspValArgAspAlaTrpGlyArgLeuProVa 116
                                                                              434
                                                                                                                      534
                                                                                                                                                                                                                                       584
                                                                                                                                                                                                                                                                                        634
                                                                                                                                                                                                                                                                                                                                           684
                                                                                                                                                                                                                                                                                                                                                                    116 lAspLeuAlaGluGluArgGlyHisArgAspValAlaGlyTyrLeuArgT 133
                                                                                                                                                                                                                                                                                                                                                                                 685 GGACTTGGCCGAGGAGCGGGGCCACCGCGACGTTGCAGGGTACCTGCGCA 734
                                                                                                       49
                                                                                                                                                           99
                                                                                                                                                                                                             83
                                                                                                                                                                                                                                                               66
                                                                                                                                                                                                                                                              17 yLeuAlaThr...ProAlaArgGlyLeuValGluLysValArgHisSerT
                                                                                                        33 rpGluAlaGlyAlaAspProAsnGlyValAsnArgPheGlyArgArgAla
                                                                                                                                                         50 IleGlnValMetMetGlySerAlaArgValAlaGluLeuLeuLeuLe
                                                                                                                                                                        66 uHisGlyAlaGluProAsnCysAlaAspProAlaThrLeuThrArgProV
                                                                                                                                                                                                                         635 CGGGCCGGGCGGCTGGACGTGCGGATGCCTGGGGGTCGTCTGCCGGT
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135
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OX ME DO
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germ-line mutation; familial melanoma locus; MLM; predisposition;
                                                                                                                                                                                                                                                                                                                                                                                                      534
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    116 lAspLeuAlaGluGluArgGlyHisArgAspValAlaGlyTyrLeuArgT 133
                                                                                                                                                                                             385 TCTGGCCAGCGCGCGCGGGGACTAGTGGAGAAGGTGCGACAGCTCC 434
                                                                                                                                                                                                                                          435 TGGAAGCCGCGCGCGGATCCCAACGGAGTCAACCGTTTCGGGAGGCGCGCG 484
                                                                                                                                                                                                                                                                                                                                     584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           685 GGACTTGGCCGAGGAGGGGGCCACCGCGACGTTGCAGGGTACCTGCGCA 734
                                                                                                                                               335 ATGCGCGAGGAGAACAAGGGCATGCCCAGTGGGGGGGGGCGCAGCGATGAGGG 384
                                                                                                                                                                     17 yLeualaThr...ProalaargGlyLeuValGluLysValargHisSerT 33
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                                                                                                                          1 MetArgGluGluAsnLysGlyMetProSerGlyGlyGlyGlySerAspGluGl 17
                                                                                                                                                                                                                                                               uHisGlyAlaGluProAsnCysAlaAspProAlaThrLeuThrArgProV
                                                                                                                                                                                                                                                                                                                          CCACGCGCGCGGACCCCAACTGCGCAGACCCTGCCACTCTCACCCGACCGG
                                                                                                                                                                                                                                                                                                                                                           83 alHisAspAlaAlaArgGluGlyPheLeuAspThrLeuValValLeuHis
                                                                                                                                                                                                                   33 rpGlualaGlyAlaaspProAsnGlyValAsnArgPheGlyArgArgAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag= a
/product= MTS2
/note= "multiple tumour suppressor"
                                Gaps: 1
Percent Identity: 95.652
                                                                                                   to: 751
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                                                                                                   Align seg 1/1 to: T69781 from: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_documentation_block:
ID V11250 standard; cDNA; 751
AC V11250;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JUL-1998 (first entry)
Human MTS2 cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              335. .751
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07 - JUN - 1995; US - 487033.

07 - JUN - 1995; US - 2487033.

18 - MAR-1994; US - 215086.

18 - MAR-1994; US - 215087.

14 - APR-1994; US - 227369.

01 - JUN - 1994; US - 227369.

17 - MAR-1995; WO - UO3316.
                  667.50
4.981
97.101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_name: N_Geneseq_36:V11250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAGCCACGGGGGAC 748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hralaThrGlyAsp 137
                                                                            US-09-016-869A-4 x T69781
                      Quality:
                                           Percent Similarity:
                                 Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
Key
CDS
         alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US5739027-A.
                                                                  alignment_block
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WHI; 98-250421/22.

DR WPI; 98-250421/22.

DR WPI; 98-250421/22.

DR WPI; 98-250421/22.

DR WPISS W40252.

PT Useful for the diagnosis of cancers related to MTSIE1-beta

PT mutation(s) and their treatment

PT mutation(s) and their treatment

Disclosure; Fig 11; 72pp; English.

CC MTS2. The MTS gene locus is also referred to as the familial melanoma

CC MTS2. The MTS gene locus, located on human chromosome 9p21. Germ line mutations

CC (MLM) genes can be used in the diagnosis of predisposition to cancers,

CC e.g. melanoma, leukaemia, astrocytoma, gliboblastoma, lymphoma, glioma,

CC Godkii's lymphoma, CLL, and cancers of the pancreas, breast, thyroid,

CC ovary, uterus, testis, kidney, stomach and rectum.

Sequence 751 BP; 130 A; 225 C; 292 G; 104 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-DEC-1998 (first entry) Coding sequence 2 of the multiple tumour suppressor MTSIEIS. Multiple tumour suppressor; MTSIEIS; human; cancer; hybridisation; somatic mutation; gene therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |||||||||:::
385 TCTGGCCAGCGCGCGGGGACTAGTGGAGAAGGTGCGACAGCTCC 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGGAAGCCGGGGGATCCCAACGGAGTCAACCGTTTCGGGAGGCGCGCG 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17 yLeuAlaThr...ProAlaArgGlyLeuValGluLysValArgHisSerT 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50 IleGlnValMetMetMetGlySerAlaArgValAlaGluLeuLeuLeuE 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATCCAGGTCATGATGATGATGACGCCCCCCGTGGCGGAGCTGCTGCTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33 rpGluAlaGlyAlaAspProAsnGlyValAsnArgPheGlyArgArgAla
                                                                                                                                                                                                                                                                                                                                                                                                                              Length: 138
Gaps: 1
Percent Identity: 95.652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to: V11250 from: 1 to: 751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_documentation_block:
ID V53831 standard; cDNA; 751 BP.
AC V53831;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_name: N_Geneseq_36:V53831
                                                                                                                                                                                                                                                                                                                                                                                                                              667.50
4.981
97.101
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US-09-016-869A-4 x V11250
                                                                                                                                                                                                                                                                                                                                                                                                                              Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
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seq_name: N_Geneseq_36:V70595
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Percent Similarity: 97.101
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US-09-016-869A-4 x V70595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 11; 73pp; English.

This is the nuclectide sequence of the multiple tumour suppressor

This is the nuclectide sequence of the invention. The MTS gene
(MTSIEIS) gene, used in the method of the invention. The MTS gene
(MTSIEIS) gene, used in the method of the invention.

This is useful in the diagnosis and prognosis of human cancer, e.g. by
standard nucleic hybridisation techniques, of patient samples. The
mutated sequences are those that are present in somatic mutations
of the gene in cancers. The vectors can be used for gene therapy
strategies to replace function of mutated protein in patients. These
can also be used to construct protein minetics, also for therapoutic
strategies. In addition the expression constructs can also be used
for recombinant production of MTS. Recombinant MTS can be used to
screen for drugs to be used for cancer therapy, and the protein
screen for drugs to be used to restore MTS function in a cell.
sequence 751 BP; 130 A; 225 C; 292 G; 104 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acids based on multiple tumour suppressor, MTS, sequences useful as hybridisation probes, primers and recombinant production of MTS in the diagnosis and treatment of cancers related to MTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100 ArgAlaGlyAlaArgLeuAspValArgAspAlaTrpGlyArgLeuProVa 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           585 recargarecreccessassecriccresacacecreseserscrecae 634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      335 ATGCGCGAGGAGAACAAGGGCATGCCCAGTGGGGGGGGGCAGCGATGAGGG 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           83 alHisAspAlaAlaArgGluGlyPheLeuAspThrLeuValValLeuHis 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MetargGluGluAsnLysGlyMetProSerGlyGlyGlySerAspGluGl 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50 IleGlnValMetMetGlySerAlaArgValAlaGluLeuLeuLe 66
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Percent Identity: 95.652
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                                                       /*tag= a
/product= "human MTS1E1S"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1 to: V53831 from: 1 to: 751
Location/Qualifiers
                                                                                                                                                                                                                                  18-MAR-1994; US-214582.

18-MAR-1994; US-215086.

18-MAR-1994; US-215087.

14-APR-1994; US-227369.

01-UN-1994; US-21938.

17-MAR-1995; WO-003316.

(MYRI-) MYRIAD GENETICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quality: 667.50 'Ratio: 4.981 nilarity: 97.101
                              335. .751
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P-PSDB; W74553.
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                                                                                                                                                                          07-JUN-1995;
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alignment_block:

mutation(s)

Kamb A;

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03-FEB-1999 (first entry)
CDNA encoding a human multiple tumour suppressor 2 (MTS2) protein.
Human; multiple tumour suppressor 1 gene; MTS1; cancer; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mouse multiple tumour suppressor gene segment - useful for primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      484
684
                                                                                                     335 ATGCGCGAGGAGAACAAGGGCATGCCCAGTGGGGGGCGCCAGCGATGAGGG 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                385 TCTGGCCAGCGCCGCGGGGGACTAGTGGAGAAGGTGCGACAGCTCC 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MetargGluGluAsnLysGlyMetProSerGlyGlyGlyGerAspGluGl
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Percent Identity: 95.652
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/*tag= b
/note= "splice site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualiflers
335. .751
/*tag= a
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                                                                                                                                                                                                                                                                                                                                                                                                      seq_documentation_block:

ID V70595 standard; cDNA; 751 BP
DT 0.7-FEB-1999 (first entry)
DE cDNA encoding a human multiple
NW Human; multiple tumour suppres
NW HUMAN; MULTIPLES
NW NOT-1995; US-8735.
NW NOTS
N
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07-JUN-1995; US-487033.
(MYRI-) MYRIAD GENETICS INC.
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338 ATGCGCGAGGAGAACAAGGCCATGCCCAGTGGGGGCGGCAGCGATGAGGG 387

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Reach DH, Demetrics DH, Bannon GJ, Serrano M;
RWPI: 95-373798/48.
P-PSDB: R85117.
New cell cycle regulating proteins bind to cyclin dependent kinase -
New cell cycle regulating proteins bind to cyclin dependent kinase -
Therapy of abnormal cell proliferation, degeneration etc.
Taim 43: Page 78: 109pp; Enquish.
C Claim 43: Page 78: 109pp; Enquish.
C CDNA (T02963) coding for the human cell-cycle regulatory (CCR)
protein pis (R85117) was identified in immunopracipitates of
transforming growth factor. The isolated cDNA can be used: to
detect mutations in CCR genes that lead to cell proliferation;
C cob preed transgent animals to study cellular disorders involving
                                                                                                                                                                                                                                                                                                                                                          01-MAR-1996 (first entry)
Cell-cycle regulatory protein p15 cDNA.
Cell-cycle regulatory protein p15: cyclin-dependent kinase inhibitor;
CCR; gene therapy; transgenic animal; cancer; cell proliferation;
                                                                                                                                                                      Ë
                                                          66
                                                                                    585 TGCATGATGCTGCCCGGGAGGCCTTCCTGGACACGCTGGTGGTGCTGCAC 634
                                                        alHisAspAlaAlaArgGluGlyPheLeuAspThrLeuValValLeuHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps: 1
Percent Identity: 94.928
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          261 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers 338. .754 /*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-APR-1994; US-227371.
25-MAY-1994; US-248812.
14-SEP-1994; US-306511.
29-NOV-1994; US-346147.
(COLD-) COLD SPRING HARBOR LAB.
                                                                                                                                                                                                                                                                                                                  _documentation_block:
T02963 standard; cDNA; 850 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           153 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 659.50
4.959
96.377
                                                                                                                                                                                                                                                                                      seq_name: N_Geneseq_36:T02963
                                                                                                                                                                                                                                               735 CAGCCACGGGGAC 748
                                                                                                                                                                                                                               133 hralaThrGlyAsp 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cells (gene therapy).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-OCT-1995.
14-APR-1995; U04636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          850 BP
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Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                      ss; ds.
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9528483-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_scores:
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                                                        83
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1 MetArgGluGluAsnLysGlyMetProSerGlyGlyGlyGlyGlySerAspGluGl 17

Align seg 1/1 to: T02963 from: 1 to: 850

alignment_block: US-09-016-869A-4 x T02963

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102964;
01-MAR-1996 (first entry)
Cell-cycle regulatory protein pl5 cDNA.
CCLI-cycle regulatory protein pl5; cyclin-dependent kinase inhibitor;
CCR; gene therapy; transgenic animal; cancer; cell proliferation;
ss; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New cell cycle regulating proteins bind to cyclin dependent kinase and related nucleic acids, antibodies etc., used in diagnosis and therapy of abnormal cell proliferation, degeneration etc. claim 43; Page 81-82; 109pp; English.

CDNA (102964) coding for the mouse cell-cycle regulatory (CCR) protein p15 (R85118) was isolated from an embryonal carcinomal library using a probe based on a mouse CCR p13;5 cDNA (T02965). The isolated cDNA can be used: to detect mutations in CCR genes that lead to cell proliferation; to breed transgenic animals to study cellular disorders involving CCR allele.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mutation/misexpression; and to correct CCR-deficient cells (gene therapy). Sequence 580 BP; 109 A; 187 C; 197 G; 87 T;
                                                                                                                                                                                                                                                                                                                                             100 ArgalaGlyalaArgLeuAspValArgAspAlaTrpGlyArgLeuProVa 116
                                                                                                                                                                                                                                                                                                                                                                                                              116 laspLeualaGluGluArgGlyHisArgAspValalaGlyTyrLeuArgT 133
537
                                                                                                                                                                                                                           637
                                                                                                                                                                                                                                                                                                                                                                              687
                                                                                                                                                                                                                                                                                                                                                                                                                                              688 GGACTIGGCCGAGGAGCGGGCCACCGCGACGTIGCAGGGTACCIGCGCA 737
                                                                     49
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                                                                                                                                                                                                                                                                         83 alHisAspAlaAlaArgGluGlyPheLeuAspThrLeuValValLeuHis 99
                                                                                                                                                        50 IleGlnValMetMetMetGlySerAlaArgValAlaGluLeuLeuLeuLe
                                                                                                                                                                                                          uHisGlyAlaGluProAsnCysAlaAspProAlaThrLeuThrArgProV
                                                                                                                                                                                                                                                                                                           588 recardarderecededadecerrecadacacecregaderecrecac
                                                                   33 rpGluAlaGlyAlaAspProAsnGlyValAsnArgPheGlyArgArgAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Beach DH, Demetrick DJ, Hannon GJ, Serrano M;
WPI; 95-373798/48.
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91. .483
/*tag= a
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14-SEP-1994; US-306511.
29-NOV-1994; US-34614.
(COLD-) COLD SPRING HARBOR LAB
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ID T02964 standard; cDNA; 580 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_name: N_Geneseq_36:T02964
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  133 hrAlaThrGlyAsp 137
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14-APR-1995; U04636.
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Mouse multiple tumour suppressor gene segment - useful for primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mouse multiple tumour suppressor 2 gene (MTS2) coding sequence. Mutine; multiple tumour suppressor 2 gene; MTS2; cancer; ss. Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                          87 laArgGluGlyPheLeuAspThrLeuValValLeuHisArgAlaGlyAla 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ArgleuAspValArgAspAlaTrpGlyArgLeuProValAspLeuAlaGl 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGGTTGGATGTGTGACGCCTGGGGCCCCTGCCGGTAGACTTGGCTGA 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GACAAGGGCATG...TTGGGCGGCAGCAGTGACGCGGGCCTGGCCACCGC 128
                                                                                                                                                                                                                         129 cececcesescaasresacescaeseseses 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        uGluArgGlyHisArgAspValAlaGlyTyrLeuArgThrAlaThrGlyA 137
                                                                                                                                       5 AsnLysGlyMetProSerGlyGlyGlySerAspGluGlyLeuAlaThr. 20
                                                                                                                                                                                                                                                     laAspProAsnGlyValAsnArgPheGlyArgArgAlaIleGlnValMet 53
                                                                                                                                                                                              21 .ProAlaArgGlyLeuValGluLysValArgHisSerTrpGluAlaGlyA 37
                                                                                                                                                                                                                                                                                                                                                                   uProAsnCysAlaAspProAlaThrLeuThrArgProValHisAspAlaA 87
                                                                                                                                                                                                                                                                                                              MetMetGlySerAlaArgValAlaGluLeuLeuLeuHisGlyAlaGl
             554.00 Length: 134
4.541 Gaps: 2
91.045 Percent Identity: 84.328
                                                                                                              to: 580
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/note= "splice site"
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1. .393
                                                                                                            from: 1
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28-JUL-1995; 058735.
28-JUL-1995; 045-508735.
07-JUN-1995; US-508735.
(MYRI-) MYRIAD GENETICS INC. Jiang P, Ramb A, Stone S; WPI: 99-044585/04.
P-PSDB; W70823.
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132. .133
/*tag= b
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: N_Geneseq_36:V70624
                                                                                                           to: T02964
                                                                  alignment_block:
US-09-016-869A-4 x T02964
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                                       Percent Similarity:
              Quality:
                          Ratio:
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alignment_scores
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                                                                                                            Align seg 1/1
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Truncated p27/p16 fusion protein encoding DNA.

Truncated p27/p16 fusion protein encoding DNA.

Truncated p27/p16 fusion protein encoding DNA.

Cyclin-dependent kinase, CDK, CDK/cyclin complex, inhibitory, restenosis;

CDK-binding motif, endothelialisation; fusion protein; therapeutic; acne; intracellular; transcettoin; fusion protein; repair; hair; smooth muscle, cardiovascular; arteriosclerotic; fibrotic disorder; cellular proliferation; rheumatoid arthritis; diabetes; cirrhosis; graft; tumour; inflammation; neurodegeneration; periodontal; spermatogenesis; tachycardia; human; p27; p16; truncated; ss.
Example 7; Fig 18; 80pp; English.

The present sequence encodes mouse multiple tumour suppressor (MTS2) gene. The MTS1 gene can be used to design primers to detect abnormalities i.e. polymorphisms which may predispose towards malignancies such as melanoma, leukaemia, astrocytoma, lymphoma, glioma, as well as tumours of e.g. the breast, thyroid, pancreas, uterus and kidneys.

Sequence 393 BP; 69 A; 124 C; 141 G; 59 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57 GGAGACGGTGCGGCAACTCCTGGAAGCCGGCGCAGATCCCAACGCCCTGA 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93 spThrLeuValValLeuHisArgAlaGlyAlaArgLeuAspValArgAsp 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       110 AlaTrpGlyArgLeuProValAspLeuAlaGluGluArgGlyHisArgAs 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 307 GCCTGGGGCCGCCTGCCGGTAGACTTGGCTGAAGAGCAGGGCCACCGTGA 356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26 lGluLysValArgHisSerTrpGluAlaGlyAlaAspProAsnGlyValA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43 snArgPheGlyArgArgAlaIleGlnValMetMetGlySerAlaArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60 ValAlaGluLeuLeuLeuLisGlyAlaGluProAsnCysAlaAspPr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          157 GTGGCAGAGCTGCTGCTCCACGGAGCAGAACCCAACTGCGCCGACCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       76 oAlaThrLeuThrArgProValHisAspAlaAlaArgGluGlyPheLeuA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length: 128
Gaps: 1
Percent Identity: 85.156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       126 pValAlaGlyTyrLeuArgThrAlaThrGlyAsp 137
                                                                                                                                                                                                                                                                                                                                                                                                                from: 1 to: 393
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                                                                                                                                                                                                                                                   Quality: 545.50
Ratio: 4.623
nilarity: 92.188
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29-JUL-1997; US-902572.
                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to: V70624
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                                                                                                                                                                                                                                                                                                Percent Similarity:
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WO9906540-A2.
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                                                                                                                                                                                                                                   alignment_scores
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Beach DH, Gyuris J, Lamphere L;

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18
                                                                                                            fibrosis and neurodegeneration

Sclaim 60; Page 83-84; 88pp: English.

Claim 60; Page 83-84; 88pp: English.

Comprision system (A) that complexes. It provides a recombinant transfection system (A) that comprises: (1) first gene construct comprision a sequence encoding an inhibitory polypeptide containing at least one CDK binding motif for binding and inhibiting activity of a CDK, linked to a transcription regulator functional in eukaryotic cells; (1) second gene construct comprising a sequence encoding a polypeptide that to promotes endothelialisation, and (11) a gene delivery composition for delivering the GCs to a cell for transfection. Also provided are nucleic consists encoding a fusion protein (FP) containing: (1) a therapeutic collusar process when FP enters the cell, and (11) a transcellular collular process when FP enters the cell, and (11) a transcellular consists of at least one CDK-binding motif and a TCP. See X26220 for consists of at least one CDK-binding mutif and a TCP. See X26210 for sequence represents a DNA encoding a human truncated p27/pl6 fusion
Fusion and chimaeric proteins including cyclin-dependent kinase binding motif - used for regulation of cell proliferation and differentiation, for treatment of, e.g. vascular injury, cancers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ë
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   626 crrcecreacrecriscoacesceseseseseseseses 675
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95 uvalvalLeuHisArgAlaGlyAlaArgLeuAspValArgAspAlaTrpG 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      876 GETGGTGCTGCACCGGGCCGGGCGCGGCTGGACGTGCGCGATGCCTGGG 925
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           526 GAAGAAAATGTITCAGACGGTGGTGGCGGGGGCCAGCGGGGGTGCGTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   576 CGCCGCGCGTGGATCCGTCGAGGATCCGGCGGCGGGGAGCAGCATGGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18 ......LeuAlaThr...ProAlaArgGlyLeuValGluLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 luLeuLeuLeuHisGlyAlaGluProAsnCysAlaAspProAlaThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        79 LeuThrArgProValHisAspAlaAlaArgGluGlyPheLeuAspThrLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45 eGlyArgArgAlaIleGlnValMetMetMetGlySerAlaArgValAlaG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           513.00 Length: 158
4.347 Gaps: 2
74.684 Percent Identity: 70.253
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Ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           317 C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           215 A;
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US-09-016-869A-4 x X26232
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Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein.
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Fusion and chimaeric proteins including cyclin-dependent kinase binding motif - used for regulation of cell proliferation and differentiation, for treatment of, e.g. vascular injury, cancers, fibrosis and neurodegeneration

Fibrosis and neurodegeneration

Claim 60; Page 85; 88pp; English.

Comprising a sequence encoding an inhibitory polypeptide containing at comprising a sequence encoding an inhibitory polypeptide containing at linked to a transcription regulator functional in eukaryotic cells; (11) comprising a sequence encoding a polypeptide that promotes endothelialisation, and (111) a gene delivery composition for delivering the GCs to a cell for transfection. Also provided are nucleic delivering the GCs to a cell for transfection. Also provided are nucleic collivaring the GCs to a cell for transfection. Also provided are nucleic collinar process when FP enters the cell, and (11) a transcellular collinar process when FP enters the cell, and (11) a transcellular consists of at least one CDK-binding motif and a TCP. See X26220 for consists of at least one CDK-binding a human truncated p27/pl6 fusion
                                                                                                                                                                                                                                                           Truncated p27/p16 fushor protein encoding DNA.

Truncated p27/p16 fushor protein encoding DNA.

Cyclin-dependent kinase: CDK: CDK/cyclin complex; inhibitory; restenosis; CDK-binding motif; endothelialisation; fusion protein; theraperitic; acne; intracellular; transcytosis; vascular wound; repair; hair; smooth muscle; cardiovascular; arteriosclerotic; fibrotic disorder; ecllular proliferation; rheumatoid arthritis; diabetes; cirrhosis; graft; tumour; infilammation; neurodegeneration; periodontal; spermatogenesis; tachycardia; human; p27; p16; truncated; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            114 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26 alGluLysvalArgHisSerTrpGluAlaGlyAlaAspProAsnGlyVal 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 GlyMetProSerGlyGlyGlySerAspGluGly.......
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Gaps: 2
Percent Identity: 75.694
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976 CGGTACCTGCGCGGGCTGCGGGG 999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Beach DH, Gyuris J, Lamphere L;
WPI; 99-153770/13.
P-PSDB; W95106.
                                                                                                                                                                    BP.
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                                                                                                                                                                                                                               25-MAY-1999 (first entry)
                                                                                                                                    seq_documentation_block:
ID X26234 standard; DNA; 782
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4.426
79.861
                                                                  seg_name: N_Geneseg_36:X26234
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29-JUL-1998; U15759.
29-JUL-1997; US-902572.
(MITO-) MITOTIX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-016-869A-4 x X26234
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WO9906540-A2.
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US-09-016-869A-4 x V11238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human MTS1 cDNA.
MTS1; multiple tumour suppressor; diagnosis; cancer; germ-line mutation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA specific for Multiple Tumour Suppressor 1E1-beta gene - are useful for the diagnosis of cancers related to MTSIE1-beta mutation(s) and their treatment Disclosure; Column 61-62; 72pp; English.

This cDNA sequence encodes a human multiple tumour suppression protein, MTS1. The MTS gene locus is also referred to as the familial melanoma (MLM) gene locus, located on human chromosome 9p21. Germ line mutations in MTS genes can be used in the diagnosis of predisposition to cancers, e.g. melanoma, leukaemia, astrocytoma, gliboblastoma, lymphoma, CLL, and cancers of the pancreas, breast, thyroid, ovary, uterus, testis, kidney, stomach and rectum.

Sequence 471 BP; 68 A; 153 C; 186 G; 64 T;
                                                                                                                                                                                                                                                               ASPThrLeuValValLeuHisArgAlaGlyAlaArgLeuAspValArgAs 109
                                                                                                                                                                                                                                                                                                                                                      palatrpGlyargLeuProValAspLeuAlaGluGluArgGlyHisArgA 126
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                    GACACGCTGGTGGTGCTGCACCGGGCCGGGGGGGCGCGGGTGGACGTGCGCGA 626
                                                                                    gValAlaGluLeuLeuLeuLeuHisGlyAlaGluProAsnCysAlaAspP 76
                                                                                                                                                                                               AsnArgPheGlyArgArgAlaIleGlnValMetMetMetGlySerAlaAr
                                                                                                             roAlaThrLeuThrArgProValHisAspAlaAlaArgGluGlyPheLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= a
/product= MTS1
/note= "multiple tumour suppressor"
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Gaps: 2
Percent Identity: 80.451
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Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                             spValAlaGlyTyrLeuArgThrAlaThrGly 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      677 AIGICGCACGGIACCIGCGCGCGGCTGCGGGG 708
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V11238 standard; cDNA; 471 BP
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18-MAR-1994; US-215686.

18-MAR-1994; US-215086.

14-APR-1994; US-215087.

14-APR-1994; US-227369.

01-JUN-1994; US-227369.

17-MAR-1995; WO-003316.

(MYRI-) MYRIAD GENETICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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4.404
86.466
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WPI; 98-250421/22.
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07-JUN-1995;
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alignment_block:

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mutation(s) Column 61-62: 73pp; English.
Claim 1; Column 61-62: 73pp; English.
This is the nucleotide sequence of the multiple tumour suppressor 1 (MTS-1) gene, used in the method of the invention. The MTS gene is useful in the diagnosis and prognosis of human cancer, e.g. by standard nucleic hybridisation techniques, of patient samples. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-DEC-1998 (first entry)
Nucleotide sequence of the CDS of the multiple tumour suppressor 1.
Multiple tumour suppressor 1; MTS-1; human; cancer; hybridisation; somatic mutation; gene therapy; ds.
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Nucleic acids based on multiple tumour suppressor, MTS, sequences useful as hybridisation probes, primers and recombinant production of MTS in the diagnosis and treatment of cancers related to MTS
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                                                                       9 ProSerGlyGlyGlySerAspGlu........GlyLeuAlaThr..
                                                                                                                 37 laAspProAsnGlyValAsnArgPheGlyArgArgAlaIleGlnValMet
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/*tag= a
/product= "human MTS-1"
to: 471
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from: 1
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ID V53819 standard; cDNA; 471
AC V53819;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_name: N_Geneseq_36:V53819
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18-MAR-1994; US-214582.
18-MAR-1994; US-215086.
18-MAR-1994; US-215087.
14-APR-1994; US-227569.
01-JUN-1994; US-251938.
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Align seg 1/1 to: V11238
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28-JUL-1995; 058735.
28-JUL-1995; US-508735.
07-JUN-1995; US-487033.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-FEB-1999 (first entry)

CDNA encoding a human multiple tumour suppressor 1 (MTS1) protein.

Human; multiple tumour suppressor 1 gene; MTS1; cancer; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          104 ArgLeuAspValArgAspAlaTrpGlyArgLeuProValAspLeuAlaGl 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120 uGluArgGlyHisArgAspValAlaGlyTyrLeuArgThrAlaThrGly 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9 ProSerGlyGlyGlySerAspGlu......GlyLeuAlaThr..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37 laAspProAsnGlyValAsnArgPheGlyArgArgAlaIleGlnValMet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70 uProAsnCysAlaAspProAlaThrLeuThrArgProValHisAspAlaA
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                                                                                                                                                                                                                                                                                                                                                                       Length: 133
Gaps: 2
Percent Identity: 80.451
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150. .151
/*tag= b
/note= "splice site"
478. .458
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/note= "splice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      from: 1
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                                                                                                                                                                                                                                                                                                                                                                                                   ): 4.404
/: 86.466
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US-09-016-869A-4 x V53819
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Truncated p27/p16 fusion protein encoding DNA.

Truncated p27/p16 fusion protein encoding DNA.

Cyclin-dependent kinase; CDK; CDK/cyclin complex; inhibitory; restenosis;
Cyclin-dependent kinase; CDK; CDK/cyclin complex; inhibitory; restenosis;
intracellular transcellular; transcytosis; vascular wound; repair; hair;
smooth muscle, cardiovascular, arteriosclerctic; fibrotic disorder;
                                                                                                                                                                                                                                                                                                                          breast,
                                                                                                                          design
Disclosure; Columns 63-66; 80pp; English.

Disclosures columns 63-66; 80pp; English.

The present sequence encodes a human multiple tumour suppressor 1 (MTS1) protein. The sequence is homologous to the corresponding murine gene. Primers designed from the gene can be used to design primers to detect abnormalities i.e. polymorphisms which may predispose towards malignancies such as melanoma, leukaemia, astrocytoma, lymphoma, glioma, as well as tumours of e.g. the breathyroid, pancreas, uterus and kidneys.

Sequence 471 BP; 68 A; 153 C; 186 G; 64 T;
                                                                                                         Mouse multiple tumour suppressor gene segment – useful for primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            laArgGluGlyPheLeuAspThrLeuValValLeuHisArgAlaGlyAla 103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  uGluArgGlyHisArgAspValAlaGlyTyrLeuArgThrAlaThrGly 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         207 GCCCAACTGCGCCGACCCGCCACCTCACCCGACCCGTGCACGACGCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37 laAspProAsnGlyValAsnArgPheGlyArgArgAlaIleGlnValMet
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Gaps: 2
Percent Identity: 80.451
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(MYRI-) MYRIAD GENETICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                         Jiang P, Kamb A, Stone S;
WPI; 99-044585/04.
P-PSDB; W80524.
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Ratio: 4.404
nilarity: 86.466
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Party 19713/10/13.

Party 19713/13.

cellular proliferation; rheumatoid arthritis; diabetes; cirrhosis; graft; tumour; inflammation; neurodegeneration; periodontal; spermatogenesis; tachycardia; human; p27; p16; truncated; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 ProSerGlyGlyGlySerAspGlu.......GlyLeuAlaThr.. 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21 .ProAlaArgGlyLeuValGluLysValArgHisSerTrpGluAlaGlyA 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37 laAspProAsnGlyValAsnArgPheGlyArgArgAlaIleGlnValMet 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54 MetMetGlySerAlaArgValAlaGluLeuLeuLeuLeuHisGlyAlaGl 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ratio: 4.404 Gaps: 2
Percent Similarity: 86.466 Percent Identity: 80.451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       267 G;
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                                                                                                                                                                                                                                       11-FEB-1999
29-JUL-1998; U15759
29-JUL-1999; US-902572.
(MITO-) MITOTIX INC.
Beach DH, Gyuris J, Lamphere L;
WPI: 99-153770/13
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Sequence
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               MAKAMA MA
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ArgLeuAspValArgAspAlaTrpGlyArgLeuDroValAspLeuAlaG1 120

893.40 893.40 893.40 893.40

451.00 451.00 451.00 451.00

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Regulatry Proteins, and Uses
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34 lualaGlyalaAspProAsnGlyValAsnArgPheGlyArgArgAlaIle 50
                                                                              seq_name: /cgn2_6/ptodata/1/ina/5D_COMB.seq:US-08-306-511A-3
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   /cgn2_6/ptodata/1/1na/5a_COMB.seq:US-08-474-177-5 + 

cgn2_6/ptodata/1/1na/5a_COMB.seq:US-08-487-033-5 + 

/cgn2_6/ptodata/1/1/1na/5b_COMB.seq:US-08-480-810-5 + 

/cgn2_6/ptodata/1/1na/5c_COMB.seq:US-08-508-735-5 +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
                                                                                                                                                                APPLICANT: Beach, David H.
APPLICANT: Beach, Douglas J.
APPLICANT: Serrano, Manuel
APPLICANT: Hannon, Gregory J.
TITLE OF INVENTION: Cell-Cycle Regulat
TITLE OF INVENTION: Related Thereto
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: CSI-001CP2
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/306,511A
FILING DATE: 14-SEP-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
                                                                                                          alignment_block:
US-09-016-869A-4 x US-08-306-511A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEO ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      837 base pairs
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Ratio: 5.234
Percent Similarity: 100.000
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MOLECULE TYPE: c
FEATURE:
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                                                                                                                                                                                                                                                                                                                           CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                      ZIP: 02109
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US-08-306-511A-3
                                                                                                                                                                                                                                                                                                                                         STATE: MA
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_scores
                                                                                                                   out_format : pfs
                                                           About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /cgn2_6/ptodata/1/1na/PCTUS_COMB.seq:PCT-US93-09945-3
OM of: US-09-016-869A-4 to: Issued_Patents_NA:*
                                                                                                                                                                                                                                                                                                         Search information block:
Query: US-09-016-869A-4
Query length: 137
Database: Issued_Patents_NA:*
Database sequences: 243080
Database length: 68777915
                                                                                                                                                                                                                                                                                                                                                                                                        Search time (sec): 85.310000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strd Orig
                              Date: Jul 21, 2000 8:07 AM
                                                                                                        Command line parameters
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67
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Sequence 3, Application US/08893274

Patent No. 596821

GENERAL INFORMATION:

APPLICANT: Beach, David H.

APPLICANT: Benetick, Douglas J.

APPLICANT: Benetick, Douglas J.

APPLICANT: Serrano, Manuel

APPLICANT: Manuel

APPLICANT: In Servano, Manuel

CORRESPENDENCE ADDRESS: 10

CORRESPENDENCE ADDRESS: 10

CORRESPENDENCE ADDRESS: 10

CORRESPENDENCE ADDRESS: 10

CORPUTES: FOLEY, HOAG & ELIOT LLP

STATE: Manuel

COMPUTES: Is Plopy disk

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COMPUTES: IS PLOPY AS A SCRICK AND AND A SCRICK AND AND A SCRICK A SCRICK AND A SCRICK A SC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           678 CITGGCCGAGGAGCGGGGCCACCGCGACGTTGCAGGGTACCTGCGCGCACA 727
428 AAGCCGCCGCGGATCCCAACGGAGTCAACCGTTTCGGGAGGCGCGCGATC 477
                                                                                                                   528 cGGCGCGGAGCCCAACTGCGCAGACCCTGCCACTCTCACCCGACCGGTGC 577
                                                                                                                                                                                                                          67 sGlyAlaGluProAsnCysAlaAspProAlaThrLeuThrArgProValH 84
                                                                           51 GlnValMetMetGlySerAlaArgValAlaGluLeuLeuLeuLeuHi 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_name: /cgn2_6/ptodata/1/ina/5D_COMB.seq:US-08-893-274-3
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117 pLeualaGluGluargGlyHisargaspValalaGlyTyrLeuargThra 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        678 CTIGGCCGAGGAGCGGGCCACCGCGACGTIGCAGGGTACCTGCGCACAG 727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51 GlnValMetMetMetGlySerAlaArgValAlaGluLeuLeuLeuLeuHi 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name: /cgn2_6/ptodata/1/ina/5A_COMB.seq:US-08-474-177-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17 yLeuAlaThrProAlaArgGlyLeuValGluLysValArgHisSerTrpG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sGlyAlaGluProAsnCysAlaAspProAlaThrLeuThrArgProValH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               528 CGGCGCGGAGCCCAACTGCGCAGACCCTGCCACTCTCACCGGACCGGTGC
                                                                                                                                                                                                                                                                                                                                                                                                               Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1 to: US-08-893-274-3 from: 1 to: 837
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIV-071.09
TELEPOMMUNICATION INFORMATION:
TELEFAX: (617) 832-1000
TELEFAX: (617) 832-7000
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 837 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_block:
US-09-016-869A-4 x US-08-893-274-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality: 717.00
Ratio: 5.234
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                     328..738
                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: CDNA FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               728 CCACGGGGGAC 738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              134 laThrGlyAsp 137
                                                                                                                                                                                                                                                                    ; NAME/KEY:
; LOCATION:
US-08-893-274-3
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11

34

117 677

577

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APPLICANT: Cannon-Albright, Lisa A.
APPLICANT: Kamb, Alexander
TITLE OF INVENTION: GERMLINE MUTATIONS IN THE MTS GENE
NUMBER OF SEQUENCES: 36
                                                                                                                         LLP
                                                                                                                                                                                                                                                                         COMPUTER KARDARLE FURNE:

KEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OMPRATING SYSTEM: PC-DOS/MS-DOS
OFFWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,177
FILING DATE: US/JUN-1995
RIDR APPLICATION NUMBER: PCT/US95/03537
FILING DATE: 17-MAR-1995
RIDR APPLICATION NUMBER: US/08/251,938
FILING DATE: 01-JUN-1994
PRIOR APPLICATION NUMBER: US/08/215,087
FILING DATE: 18-MAR-1994
PRIOR APPLICATION NUMBER: US/08/215,086
FILING DATE: 18-MAR-1994
PRIOR APPLICATION NUMBER: US/08/215,086
FILING DATE: 18-MAR-1994
PRIOR APPLICATION NUMBER: US/08/215,086
FILING DATE: 18-MAR-1994
PRIOR APPLICATION NUMBER: US/08/217,369
FILING DATE: 14-APR-1994
PRIOR APPLICATION NUMBER: US/08/214,582
FILING DATE: 11-APR-1994
APPLICATION NUMBER: US/08/214,582
FILING DATE: 11-APR-1994
ANTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey.
REGISTRATION NUMBER: 28,957
REFERENDE/POCKET NUMBER: 28,957
REFERENDE/POCKET NUMBER: 28,957
                                                                                                        ADDRESSEE: Venable, Baetjer, Howard & Civiletti,
STREET: 1201 New York Avenue, Suite 1000
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps: 1
Percent Identity: 95.652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: US-08-474-177-15 from: 1 to: 751
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TELEPHONE: 202-962-4810
TELEFAX: 202-962-4830
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 751 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                          STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                667.50
4.981
97.101
                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDS
335..751
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MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Quality:
Ratio:
Percent Similarity:
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ORIĞINAL SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; NAME/KEY:
; LOCATION:
US-08-474-177-15
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1 MetArgGluGluAsnLysGlyMetProSerGlyGlyGlySerAspGluGl 17

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385 TCTGGCCAGCGCGGGGGGGACTAGTGGAGAAGGTGCGACAGGTCC 434
                                                                                                                                                585 recardarecreccessasserrecresacacscresresrecres 634
                                                                                                                                                                                               50 IleGlnValMetMetMetGlySerAlaArgValAlaGluLeuLeuLeuLe 66
                                                                                                                                                                                                                                                                                                                                                alHisAspAlaAlaArgGluGlyPheLeuAspThrLeuValValLeuHis 99
                                                     17 yLeuAlaThr...ProAlaArgGlyLeuValGluLysValArgHisSerT 33
                                                                                                                           33 rpGluAlaGlyAlaAspProAsnGlyValAsnArgPheGlyArgArgAla 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_name: /cgn2_6/ptodata/1/ina/5B_COMB.seq:US-08-487-033-15
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COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,033
FILING DATE: US/08/487,033
FILING DATE: US/08/487,033
FILING DATE: 17-MAR-1995
PRIOR APPLICATION NUMBER: ROS 08/251,938
FILING DATE: 17-MAR-1995
PRIOR APPLICATION NUMBER: US 08/251,938
FILING DATE: US-JUN-1994
PRIOR APPLICATION NUMBER: US 08/215,087
FILING DATE: B-MAR-1994
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APPLICATION NUMBER: US 08/215,087
FILING DATE: B-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,086
FILING DATE: B-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,086
FILING DATE: B-MAR-1994
PRIOR APPLICATION DATA:
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735 CAGCCACGGGGGAC 748

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100 ArgAlaGlyAlaArgLeuAspValArgAspAlaTrpGlyArgLeuProVa 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        83 alHisAspAlaAlaArgGluGlyPheLeuAspThrLeuValValLeuHis 99
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Percent Identity: 95.652
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APPLICATION NUMBER: US 08/227,369
FILING DATE: 14-APR-1994
PRIOR APPLICATION NUMBER: US 08/214,582
APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Inhen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24,884-109348-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-8300
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 751 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CONA
HYPOTHETICAL: NO
ANTI-SENSE: NO
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US-09-016-869A-4 x US-08-487-033-15
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ORIGINAL SOURCE:
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               667.50
4.981
97.101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hrAlaThrGlyAsp 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                 ; LOCATION:
US-08-487-033-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_scores:
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CURRENT APPLICATION DATA:

SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,810
FILING DATE: 07-JUN 1995
FILON APPLICATION NUMBER: US/08/480,316
FILING DATE: 17-MAR-1995
PRIOR APPLICATION NUMBER: US/08/251,938
FILING DATE: 17-MAR-1995
PRIOR APPLICATION NUMBER: US 08/251,938
FILING DATE: 01-JUN-1994
PRIOR APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-MAR-1994
PRIOR APPLICATION NUMBER: US 08/215,086
FILING DATE: 18-MAR-1994
PRIOR APPLICATION NUMBER: US 08/215,086
FILING DATE: 14-APR-1994
PRIOR APPLICATION NUMBER: US 08/215,086
FILING DATE: 14-APR-1994
PRIOR APPLICATION NUMBER: US 08/215,589
FILING DATE: 14-APR-1994
PRIOR APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-MAR-1994
PRIOR APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-MAR-1994
ATTONINEY/AGENT INFORMATION:
AMAR: Therm Jeffron I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Identity: 95.652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24884-109348
                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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REGISTRATION NUMBER: 28,957
REFERENCE/COCKET UNBER: 24,
TELECOMMUNICATION:
TELEPHONE: 202-962-4810
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TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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4.981
97.101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: CDNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORIGINAL SOURCE
                                                                                                                                                                                                                                                                                                COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; LOCATION:
US-08-480-810-15
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seq_documentation_block:
    Sequence 15, Application US/08508735
    Patent No. 5843756
    GENERAL INFORMATION:
    APPLICANT: Stone, Steven
    APPLICANT: Stone, Ping
    APPLICANT: Mamb, Alexander
    ITTLE OF INVENTION AN ENGINE AND THERAPEUTIC USE THEREOF
    CORRESPONDENCES: 47
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
    STREET: 1201 New York Avenue, Suite 1000
    COUNTRY: Washington
    STATE: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |||||||||||:::
385 TCTGGCCAGCGCGCGGGGGACTAGTGGAGAAGGTGCGACAGCTCC 434
                                                                                                                                                                                                                                                            585 recardarecrecceseasecricereaacaccresresrecrecre 634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            116 lAspLeuAlaGluGluArgGlyHisArgAspValAlaGlyTyrLeuArgT 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 685 GGACTTGGCCGAGGAGCGGGGCCACCGCGACGTTGCAGGGTACCTGCGCA 734
                                                                                                                                                                                                                                                                                                                                           17 yLeuAlaThr...ProAlaArgGlyLeuValGluLysValArgHisSerT 33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83 alHisaspalaalaargGluGlyPheLeuAspThrLeuValValLeuHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/508,735 FILING DATE:
                                                           from: 1 to: 751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US to be assigned
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 20005
COMPUTER REARABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                           Align seg 1/1 to: US-08-480-810-15
alignment_block:
US-09-016-869A-4 x US-08-480-810-15
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83 alHisAspalaalaArgGluGlyPheLeuAspThrLeuValValLeuHis 99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length: 138
Gaps: 1
Percent Identity: 95.652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to: US-08-508-735-15 from: 1 to: 751
                                                     NAME: Tinen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REPERENCE DOCKET NUMBER: 2484-109348
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4848
TELEPHONE: 202-962-4848
TELEPHONE: 7202-962-8300
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 751 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TYPE: nucleic acid
STRANDEDNESS: double
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature;
COCATION: 490..491

COTHER INFORMATION: /note= "Splice site"

NS-08-508-735-15
APPLICATION NUMBER: PCT/US95/03316
FILING DATE: 17-MAR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_block:
US-09-016-869A-4 x US-08-508-735-15
                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality: 667.50
Ratio: 4.981
nilarity: 97.101
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FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                           ORIGINAL SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_scores
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133 hralaThrGlyAsp 137

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seq_documentation_block:

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sequence 15, Application US/08486047

patent No. 5994095

GENERAL INFORMATION:

APPLICANT: Kamb, Alexander

TITLE OF INVENTION: MTS2 GENE

NUMBER OF SEQUENCES: 36

CORRESPONDENCE ADDRESS:

ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP

STREET: 1201 New York Avenue, Suite 1000

CITY: Washington

STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17 yLeualathr...ProalaargGlyLeuValGluLysValargHisSert 33
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385 TCTGGCCAGCGCGGGGGGGACTAGTGGAGAAGGTGCGACAGCTCC 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      116 lAspLeuAlaGluGluArgGlyHisArgAspValAlaGlyTyrLeuArgT 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       685 GGACTIGGCCGAGGAGCGGGCCCACCGCGACGTIGCAGGGTACCTGCGCA 734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           83 alHisAspAlaAlaArgGluGlyPheLeuAspThrLeuValValLeuHis 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66 uHisGlyAlaGluProAsnCysAlaAspProAlaThrLeuThrArgProV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50 IleGlnValMetMetGlySerAlaArgValAlaGluLeuLeuLe
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Gaps: 1
Percent Identity: 95.652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,047
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                            to: 751
                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to: US-08-848-251-15 from: 1
                                                                                                                                                                                                                                                                                                                                                             US-09-016-869A-4 x US-08-848-251-15
                                                                                                                                                 667.50
4.981
97.101
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                                                                                                                                                                                                   Ratio:
                                                                                                                                                                                                                                    Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 20005
                                                                                                                    alignment_scores
US-08-848-251-15
                                                                                                                                                                                                                                                                                                                       alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        335
                                                                                                            Sequence 15, Application US/08848251

Sequence 15, Application US/08848251

Patent No. 5980815

Sequence 15, Application US/08848251

Sequence 15, Application US/08848251

SEQUENCE:

APPLICANT: Cannon-Albright, Lisa A. APPLICANT: Cannon-Albright, Lisa A. APPLICANT: Ramb, Alexander

TITLE OF INVENTION: GERMILNE MUTATIONS IN THE WTS GENE AND

TITLE OF INVENTION: GENE

NUMBER OF SEQUENCES: 36

CORRESPONDENCE ADDRESS: 36

CORRESPONDENCE ADDRESS: 36

CORRESPONDENCE ADDRESS: 36

CONTRY: USA

ILP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: FLORDY disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

COMPUTER: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION NUMBER: US/08/848,251

FILING DATE:

FILING DA
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/474,083
FILING DATE: 07-001-1995
APPLICATION NUMBER: PCT/US95/03537
FILING DATE: 17-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,938
FILING DATE: 01-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,086
FILING DATE: 18-MAR-1994
PRIOR APPLICATION UNMERR: US 08/217,369
FILING DATE: 14-MAR-1994
PRIOR APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: INDOM NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 28,957
REFERENCE/STATION NUMBER: 28,957
REFERENCE/STATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 28,957
REFERENCE/STATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 28,957
REFERENCE/STATION NUMBER: 28,957
REFERENCE/STATI
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SEQUENCE CHARACTERISTICS:
LENGTH: 751 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
                                     735 CAGCCACGGGGGAC 748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: CDS
LOCATION: 335..751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORIGINAL SOURCE
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17 yLeuAlaThr...ProAlaArgGlyLeuValGluLysValArgHisSerT 33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50 IleGlnValMetMetMetGlySerAlaArgValAlaGluLeuLeuLe 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps: 1
Percent Identity: 95.652
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/03316
FILING DATE: 17-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,938
FILING DATE: 01-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,086
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/214,589
FILING DATE: 14-APR-1994
PRIOR APPLICATION NUMBER: US 08/214,582
FILING DATE: 14-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: INHOME US 08/214,582
FILING DATE: 18-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: INHOME US 08/214,582
FILING DATE: 18-MAR-1994
ATTORNEY/AGENT INFORMATION:
TELECOMMUNICATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 28,957
RELEBRAN: 202-962-8300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 202-962-8300
INFORMATION FOR SEQ 1D NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 751 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_block:
US-09-016-869A-4 x US-08-486-047-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORIGINAL SOURCE:
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4.981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: CDNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_scores:
   Quality: Ratio:
   Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; NAME/KEY:
; LOCATION:
US-08-486-047-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ANTI-SENSE:
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Sequence 15, Application US/09120130

Patent No. 603746

GENERAL INFORMATION:

APPLICANT: Kamb, Alexander

TITLE OF INVENTION: MTSI GENE

NUMBER OF SEQUENCES: 36

CORRESPONDENCE ADDRESS:

ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP

STREET: 1201 New York Avenue, Suite 1000

CITY: Washington

STATE: DC
100 ArgAlaGlyAlaArgLeuAspValArgAspAlaTrpGlyArgLeuProVa 116
                                                                                                                  seq_name: /cgn2_6/ptodata/1/ina/6_COMB.seq:US-09-120-130-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 ADELICATION DATA: ADELICATION NUMBER: US/09/120,130 FILLING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PFILING DATA:

APPLICATION DATA:
APPLICATION NUMBER: US 08/251,938
FILING DATE: 01-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-MAR-1994
FILING DATE: 18-MAR-1994
FILING APPLICATION NUMBER: US 08/215,086
FILING APPLICATION DATA:
APPLICATION NUMBER: US 08/227,369
FILING DATE: 18-MAR-1994
FILING DATE: 18-MAR-1994
APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Innen, Jeffrey L.
RECISTRATION NUMBER: 28,957
RECISCOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-62-4810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/480,810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 751 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                202-962-8300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                          133 hralaThrGlyAsp 137
                                                                                                                                                                                                                                                                                                                                                                                                     seq_documentation_block
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
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534
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APPLICANT: Kamb, Alexander
APPLICANT: Kamb, Alexander
TITLE OF INVENTION: MTS1 GENE
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
CITY: Mashington
STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_name: /cgn2_6/ptodata/1/ina/6_COMB.seq:US-09-115-252-15
                                                                                                                                                                 Percent Identity: 95.652
                                                                                                                                                                                                                             from: 1 to: 751
                                                                                                                                         Length:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_documentation_block:
; Sequence 15, Application US/09115252
; Patent No. 6060301
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                                                                                                                                                                                         alignment_block:
US-09-016-869A-4 x US-09-120-130-15
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
                                                                                                                                      667.50
4.981
97.101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 20005
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     133 hralaThrGlyAsp 137
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335..751
                                                                                                                           alignment_scores:
Quality:
Ratio:
                                                                                                                                                               Percent Similarity:
                                                              ; NAME/KEY:
; LOCATION:
US-09-120-130-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                  FEATURE:
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33 rpGluAlaGlyAlaAspProAsnGlyValAsnArgPheGlyArgArgAla 49
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to: US-09-115-252-15 from: 1 to: 751
                                                                                                                                                                                                                  FILLING DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/480,810
FILING DATE: U7-01955
APPLICATION NUMBER: PCT/US95/0316
FILING DATE: 17-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,938
FILING DATE: 01-7011994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,086
FILING DATE: 14-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/217,369
FILING DATE: 14-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REEFERDORE: 202-962-4810
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/115,252
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_block:
US-09-016-869A-4 x US-09-115-252-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORIGINAL SOURCE:
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           751 base pairs
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4.981
97.101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDS
335..751
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; LOCATION:
US-09-115-252-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_scores
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seq_documentation_block:
    Sequence 3, Application US/08627610
    Patent No. 5919997
    GENERAL INFORMATION:
    APPLICANT: Beach, David H.
    APPLICANT: Serrano, Manuel.
    APPLICANT: Depinho, Ronald.
    TITLE OF INVENTION: Transgenic Animals Having Modified Cell-Cycle TITLE OF INVENTION: Regulation
    NUMBER OF SEQUENCES: 13
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: LAHIVE & COCKFIELD
                                                                                                                                                                                                        634
                                                                                                                                                                                                                                                                                       684
                                                                                                                                                                                                                                                                                                                                                      685 GGACTIGGCCGAGGAGGGGCCACCGCGACGTIGCAGGGTACCTGCGCA 734
                                                                                   83
100 ArgAlaGlyAlaArgLeuAspValArgAspAlaTrpGlyArgLeuProVa
                                                                                                                                                                                                                                                                                                                           116 lAspLeuAlaGluGluArgGlyHisArgAspValAlaGlyTyrLeuArgT
                                                                                                                                                                                                                                                                   83 alHisAspAlaAlaArgGluGlyPheLeuAspThrLeuValValLeuHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_name: /cgn2_6/ptodata/1/ina/5D_COMB.seq:US-08-627-610-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION UNBER: 35.709
REFERENCE/DOCKET NUMBER: CSI-001CP6
TELECOMMUNICATION INFORMATION:
TELECHAN: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 850 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION NOMBER: US/08/627,610
FILING DATE: 04-APR-1996
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: LAHIVE & COCKFIELD STREET: 60 State Street CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                   735 CAGCCACGGGGGAC 748
                                                                                                                                                                                                                                                                                                                                                                                                            133 hralathrGlyAsp 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ) NAME/KEY: CDS
; LOCATION: 338.751
US-08-627-610-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
```

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seq_documentation_block:
Sequence 3, Application US/08581918A
Patent No. 6043030
GENERAL INFORMATION:
APPLICANT: Beach, David H.
APPLICANT: Benetrick, Douglas J.
APPLICANT: Benetrick, Manuel
APPLICANT: Applicant, Gregory J.
TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses
TITLE OF INVENTION: Related Thereto
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       116 lAspLeuAlaGluGluArgGlyHisArgAspValAlaGlyTyrLeuArgT 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17 yLeuAlaThr...ProAlaArgGlyLeuValGluLysValArgHisSerT 33
                                                                                                                                                                                                                                                                                                                                                            50 IleGlnValMetMetGlySerAlaArgValAlaGluLeuLeuLe 66
                                                                                                                                                              1 MetArgGluGluAsnLysGlyMetProSerGlyGlyGlySerAspGluGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_name: /cgn2_6/ptodata/1/ina/6_COMB.seq:US-08-581-918A-3
                                              Percent Identity: 95.652
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/581,918A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Foley, Hoag & Eliot
STREET: One Post Office Square
                                                                              alignment_block:
US-09-016-869A-4 x US-08-627-610-3
             667.50
4.981
97.101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              133 hralaThrGlyAsp 137
               Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Boston STATE: MA
alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
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1 MetargGluGluAsnLysGlyMetProSerGlyGlyGlySerAspGluGl 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps: 1
Percent Identity: 95.652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to: US-08-581-918A-3 from: 1 to: 850
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,371
FILING DATE: 14-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/154,915
FILING DATE: 18-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/991,997
FILING DATE: 17-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIV-071.06
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAX: (617) 832-1299
TELEFRAX: (617) 832-1299
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 850 base pairs
TYPE: nucleic acid
STRANDEDIESS: both
          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNDERS:
TLING DATE: 30-UN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/346,147
FILING DATE: 29-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/306,511
FILING DATE: 14-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/248,812
APPLICATION NUMBER: US 08/248,812
APPLICATION NUMBER: US 08/248,812
APPLICATION NUMBER: US 08/248,812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_block:
US-09-016-869A-4 x US-08-581-918A-3
02-JAN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_scores:
Quality: 667.50 |
Patfo: 4.981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97.101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: CDNA FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        338..751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; NAME/KEY:
; LOCATION:
US-08-581-918A-3
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TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses TITLE OF INVENTION: Related Thereto
NUMBER OF SEQUENCES: 10
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                   seq_name: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:PCT-US95-04636-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    637
Gaps: 1
Percent Identity: 95.652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to: PCT-US95-04636-3 from: 1 to: 850
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/346,147
FILING DATE: 29-NOV-1994
PRIOR APPLICATION NUMBER: US 08/306,511
FILING DATE: 14-SEP-1994
PRIOR APPLICATION NUMBER: US 08/248,812
FILING DATE: 15-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/248,812
FILING DATE: 14-APP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,371
FILING DATE: 14-APP-1994
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH 880 DASE PAIRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04636
                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application PC/TUS9504636
GENERAL INFORMATION:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_block:
US-09-016-869A-4 x PCT-US95-04636-3
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4.981
97.101
                                                                                                                                                                                                                             133 hrAlaThrGlyAsp 137
                                                                                                                                                                                                                                                                  738 CAGCCACGGGGGAC 751
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338..751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                               seq_documentation_block;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; NAME/KEY:
; LOCATION:
PCT-US95-04636-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_scores:
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CDS
91..480
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; LOCATION:
US-08-627-610-7
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NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   479 AT 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Serrano, Manuel
APPLICANT: Serrano, Manuel
APPLICANT: Beach, Bandd H.
APPLICANT: Depinho, Ronald A.
TITLE OF INVENTION: Transgenic Animals Having Modified Cell-Cycle
TITLE OF INVENTION: Regulation
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
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                       438 TGGAAGCCGGCGCGCATCCCAACGGAGTCAACCGTTTCGGGAGGCGCGCG 487
                                                                                        33 rpGlualaGlyalaAspProAsnGlyValAsnArgPheGlyArgArgAla 49
                                                                                                                                                                                                                                                                                                                                                                   83 alHisAspAlaAlaArgGluGlyPheLeuAspThrLeuValValLeuHis 99
17 yLeuAlaThr...ProAlaArgGlyLeuValGluLysValArgHisSerT 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_name: /cgn2_6/ptodata/1/1na/5D_COMB.seq:US-08-627-610-7
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC comparatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATE: US/08/627,610
FILING DATE: 04-APR-1996
CLASSIFCATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION UNMBER: 36,709
REFERENCE/DOCKET NUMBER: GSI-001CP6
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION FOR SEQ ID NO: 7:
SEGNENCE CHRACATERISTICS:
LENGTH: 580 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_documentation_block:
    Sequence 7, Application US/08627610
    Patent No. 5919997
    GENERAL_INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 133 hralaThrGlyAsp 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
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GENERAL INFORMATION:
APPLICANT: Beach, David H.
APPLICANT: Demetrick, Douglas J.
APPLICANT: Serrano, Manuel
APPLICANT: Hannon, Gregory J.
TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses
TITLE OF INVENTION: Related Thereto
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            129 ATGATGGGCAGGCCAGGGTGGCAGAGCTGCTGCTCCACGAGGAGA 278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       329 CTCGGGAAGGCTTCCTGGACACGCTTGTCGTGCTGCACCGGGCAGGGGCG 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   104 ArgLeuAspValArgAspAlaTrpGlyArgLeuDroValAspLeuAlaG1 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120 uGluArgGlyHisArgAspValAlaGlyTyrLeuArgThrAlaThrGlyA 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         129 CGCGGCGCGGGGCAAGTGGAACGGTGCGGCAGCTCCTGGAAGCCGGCG 178
                                                                                                                                                                                                                                                                                                                                                                                                    37 laAspProAsnGlyValAsnArgPheGlyArgArgAlaIleGlnValMet 53
                                                                                                                                                                                                                                                                                                            21 .ProAlaArgGlyLeuValGluLysValArgHisSerTrpGluAlaGlyA 37
                                                                                                                                                                                                                                                                                                                                                                                                                                    179 CAGATCCCAACGCCCTGAACCGCTTCGGGAGGCGCCCAATCCAGGTCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54 MetMetGlySerAlaArgValAlaGluLeuLeuLeuLeuHisGlyAlaGl
                                                                                                                                                                                                               5 AsnLysGlyMetProSerGlyGlyGlySerAspGluGlyLeuAlaThr..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_name: /cgn2_6/ptodata/1/ina/6_COMB.seq:US-08-581-918A-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_documentation_block:
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; Patent No. 6043030
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US-09-016-869A-4 x US-08-627-610-7
554.00
4.541
91.045
  Quality:
Ratio:
                                            Percent Similarity:
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5 AsnLysGlyMetProSerGlyGlyGlySerAspGluGlyLeuAlaThr.. 20 :::||||||||||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21 .ProAlaArgGlyLeuValGluLysValArgHisSerTrpGluAlaGlyA 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MetMetGlySerAlaArgValAlaGluLeuLeuLeuLeuHisGlyAlaGl 70
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91.045 , Percent Identity: 84.328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: VINCENT, MATCHEW P.

REGISTRATION NUMBER: 36,709

REFERENCE/DOCKET NUMBER: MIV-071.06

TELEPHONE: (617) 832-1299

INFORMATION FOR SEQ ID NO: 7

SEQUENCE CHARACTERISTICS:

LENGTH: 580 base pairs
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SOFTWARE:
WOLDEAG
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/581,918A
FILING DATE: 02-JAN-1996
CLASSIFICATION A435
REIGN APPLICATION DATA:
APPLICATION NUMBER: US 08/497,214
FILING DATE: 30-JUN-1995
REIGN APPLICATION DATA:
APPLICATION NUMBER: US 08/36,147
FILING DATE: 29-NOV-1994
PRIOR APPLICATION NUMBER: US 08/36,511
FILING DATE: 14-SEP-1994
PRIOR APPLICATION NUMBER: US 08/26,511
FILING DATE: 25-MAY-1994
PRIOR APPLICATION NUMBER: US 08/27,371
APPLICATION NUMBER: US 08/27,371
APPLICATION NUMBER: US 08/227,371
FILING DATE: 14-APR-1994
PRIOR APPLICATION NUMBER: US 08/154,915
FILING DATE: 18-NOV-1993
PRIOR APPLICATION NUMBER: US 08/154,915
FILING DATE: 17-DEC-1992
FILING DATE: 17-DEC-1992
ATTORNEY-AGENT INFORMATION:
APPLICATION NUMBER: US 07/991,997
FILING DATE: 17-DEC-1992
ATTORNEY-AGENT INFORMATION:
APPLICATION NUMBER: US 07/991,997
FILING DATE: 17-DEC-1992
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDS
91..480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality:
Ratio:
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; LOCATION:
US-08-581-918A-7
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NCI_CGAP NCI_CGAP NCI_CGAP NCI_CGAP

ts72d01.x1 b w150c04.x1 b qk47d01.x1 b wh90g02.x1

AI916967 1 AI869175 v AI280899 c AI762172 v

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LOCUS A1394605 566 bp mRNA EST 30-MAR-1999
DEFINITION 1913905.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2108696 3'
SIMILIAT TO SW:CDN2_HUMAN P42771 CYCLIN-DEPENDENT KINASE 4 INHIBITOR A : contains LTR9.b3 TAR1 repetitive element ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 566)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. 566
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/clone="IMAGE:2108696"
/clone="IMAGE:2108696"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length: 92
Gaps: 0
Percent Identity: 91.304
    6.3e-15
6.9e-15
8.7e-15
1.2e-14
  426.52
425.81
423.98
421.63
                                                                                                                                                                                                                                                                                                     AI394605.1 GI:4224152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_block:
US-09-016-869A-4 x AI394605/rev
  226.00
226.00
225.00
223.00
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94.565
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                                                                                                                   seq_name: gb_est20:AI394605
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  gb_est27:AI916967
gb_est26:AI869175
gb_est18:AI280899
gb_est25:AI762172
                                                                                                                                                                                                                                                                                                                                                       human.
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AW324496 4502h12.x1 NIH_MCC_4 I
AR871381 w181d11.x1 NCI_CGAP_BI
AI87381 w181d11.x1 NCI_CGAP_BI
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AI88362 w237061.x1 NCI_CGAP_BI
AI8633790 tt28e10.x1 NCI_CGAP_BI
AI8633790 tt28e10.x1 NCI_CGAP_BI
AI8633790 tt28e10.x1 NCI_CGAP_BI
AM631790 w23706.x1 NCI_CGAP_BI
AM631770 tr28e10.x1 NCI_CGAP_BI
AM651373 m174b05.x1 NCI_CGAP_BI
AM657137 m174b05.x1 NCI_CGAP_BI
AA857137 m174b05.x1 NCI_CGAP_BI
AM818639 x21706.x1 NCI_CGAP_CI
AM818639 x115e01.x1 NCI_CGAP_CI
AM9190459 x115e01.x1 NCI_CGAP_CI
AM169901 x134d12.x1 NCI_CGAP_CI
AI70354 w493c07.x1 NCI_CGAP_CI
AI70354 w493c07.x1 NCI_CGAP_CI
AI70354 w493c07.x1 NCI_CGAP_CI
AI69901 x134d12.x1 SOBIES_NFI
AI69901 x134d12.x1 SOBIES_NFI
AI69901 x134d12.x1 SOBIES_NFI
AI69901 x134d12.x1 SOBIES_NFI
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AI656826 tt54C09.x1 NCI_CGAP_LU
AI568350 mg21d06.x1 NCI_CGAP_LU
AI568350 mg21d06.x1 NCI_CGAP_LU
AI568350 mg21d06.x1 NCI_CGAP_LU
                                                                                                                                                                             About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
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88.10.07c  
88.10.
OM of: US-09-016-869A-4 to: EST:*
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Query: US-09-016-869A-4
Query length: 137
Database: EST:*
Database sequences: 5247842
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Search time (sec): 1223.270000
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gb_est26:AI871381
gb_est26:AI870879
gb_est17:AI198233
gb_est19:AI362049
gb_est25:AI765996
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gb_est21.A1499733
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Align seg 1/1 to: AW328496
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US-09-016-869A-4 x AW328496
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LOCUS AI871381
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I (bases 1 to 648)

NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.

National Institutes of Health, Mammalian Gene Collection (MGC)

L Unpublished (1999)

On Apr 7, 1998 this sequence version replaced gi:3036295.

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert_Strausbergenih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Edge BioSystems

CDNA Library Preparation: Edge BioSystems

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: NIH Intramural Sequencing Center (NISC)

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.lnl.gov/bbrp/image/image.html

Plate: LLCM0030 row: 0 column: 24

Seq primer: -21M13 forward primer (ABI).
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//ab_host="DH10B (phage-resistant)"
//ab_host="DH10B (phage-resistant)"
//note="Organ: Cervix; Vector: pOTB/a; Site_l: Scel;
Site_2: Ceul: cDNA made by oligo-dT priming.
Directionally cloned into Ceul/Scel sites using the Directionally cloned into Ceul/Scel sites using the Directionally cloned into Ceul/Scel sites using the Directionally cloned into Ceul/Scel sites and 3' adaptor: taactatacaggiccaaggiaggiaggiagator: titcattacctctttctccgcaccccacataaa. Average adaptor: titcattacctctttctccgcaccccacataaa. Average
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AW328496 648 bp mRNA EST 28-JAN-2000 ds02h12.x1 NIH_MGC_4 Homo sapiens cDNA clone IMAGE:2847599 5', mRNA
                                                                                                                                                                                            516 GGAGCTGCTGCTCCACGGCGCGGAGCCCAACTGCGCNGACCCCGCCA 467
                                                                                                                                                                                                                                                                                               pGlyArgLeuProValAspLeuAlaGluGluArgGlyHisArgAspValA 128
                                                                                                                                                                                                                                                                                                                                               366 GGGCCGTCTGCCCGTGGACCTGAGGAGCTGGGCCATCGCGATGTCG 317
                                                                                                                                              466 CTCTCACCCGACCCGTGCACGCTGCCCGGGAGGGCTTCCTGGACACG 417
61 aGluLeuLeuLeuLeuHisGlyAlaGluProAsnCysAlaAspProAlaT 78
                                                                                           78 hrLeuThrargProvalHisAspalaAlaArgGluGlyPheLeuAspThr 94
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    .648
    /organism="Homo sapiens"

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/clone_lib="NIH_MGC_4"
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A1871381 590 bp mRNA EST 07-MAR-2000 w181d11.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2431317 3' similar to TR:Q16361 Q16361 CELL CYCLE NEGATIVE REGULATOR BETA FORM ', mRNA sequence.

A1871381.1 G1:5545430
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CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

Www.Pio.llnl.gov/bbrp/image/image.html

Insert Length: 845 Std Error: 0.00
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Email: Robert_Strausbergenih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mammalia; Butheria; Primates; Craniata; Vertebrata; Euteleostoml; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 590)

NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute / National Institute of Neurological Josocders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/PRGAP), Tumor Gene Index

Unpublished (1998)

On Oct 30, 1998 this sequence version replaced gi:3813427.
                                                                                                                                                                                                                                                                                                                        263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       119 laGluGluArgGlyHisArgAspValAlaGlyTyrLeuArgThrAlaThr 135
                                                                                    86 AlaAlaArgGluGlyPheLeuAspThrLeuValValLeuHisArgAlaGl 102
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                                                                                                                                                                                                                                                                                          85
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                                                      36 GlyAlaAspProAsnGlyValAsnArgPheGlyArgArgAlaIleGlnVa
                                                                                                                                                                         52 IMetMetGlySerAlaArgValAlaGluLeuLeuLeuLeuHisGlyA
                                                                                                                                                                                                                                                                                          69 laGluProAsnCysAlaAspProAlaThrLeuThrArgProValHisAsp
from: 1 to: 648
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/organism="Homo sapiens"
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High quality sequence stop: 4
Location/Qualifiers
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A187/08/3 J.7 a.M. MINAMAN WAITAGIL XI NCI_CGAP_BRIDS Homo sapiens CDNA clone IMAGE:2430933 3/
similar to TR:Q1G361 Q16361 CELL CYCLE NEGATIVE REGULATOR BETA FORM
1, mRNA sequence.
A187/0879.1 GI:5544847
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bummalla: Eutherla: Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 579)
NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index
Unpublished (1998)
On May 18, 1998 this sequence version replaced gi:3136859.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             67
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5.000 Gaps: 0
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KEYWORDS
SOURCE
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CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/thmage.html
Insert Length: 819 Std Error: 0.00
Seq primar: -400P from Gibco
High quality sequence stop: 474.
Location/Qualifiers
I. 579

// Clone—"Homo sapiens"
// Ab_xref="taxon: 9666"
// Clone—"InAGE: 243093"
// Clone—"InAGE: 243093"
// Lab_not="hubbalastic oligodendroglioma"
// Lab_not="hubbalastic oligodendroglioma"
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
19-1: (301) 496-1550
Emall: Robert Strausbergfaith.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84 isaspalaalaargGluGlyPheLeuaspThrLeuValValLeuHisarg 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 455 ACGACGCTGCCCGGGAGGGCTTCCTGGACACGCTGGTGGTGCTGCACCGG 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pLeuAlaGluGluArgGlyHisArgAspValAlaGlyTyrLeuArgThrA 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67 sGlyAlaGluProAsnCysAlaAspProAlaThrLeuThrArgProValH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51 GlnValMetMetGlySerAlaArgValAlaGluLeuLeuLeuHi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to reverse of: AI870879 from: 1 to: 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length: 86
Gaps: 0
Percent Identity: 93.023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-016-869A-4 x AI870879/rev
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4.976
95.349
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DEFINITION

ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

REFERENCE AUTHORS

TITLE

JOURNAL COMMENT

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A1362049 580 bp mRNA EST 15-FEB-1999 gy39f07.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2014405 3' similar to TR:Q16361 Q16361 CELL CYCLE NEGATIVE REGULATOR BETA FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: Robert_Strausberg@nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 580)
NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurological Josofders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAR); Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bonaldo, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Seq

Clone distribution: NCI-CGAP clone distribution inf

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.qov/Dbrp/image/image.html

Insert Length: 884 Std Error: 0.00

Seq primer: -400P from Gibco

High quality sequence stop: 321.

Location/Qualifiers
                                                                                                                                           107 largaspalaTrpGlyargLeuproValaspLeualaGluGluArgGlyH 124
                                                                                                                                                                                           385 GCGCGATGCCTGGGGCCGTCTGCCCGTGGACCTGGCTGAGGAGCTGGGCC 336
                                                91 PheLeuAspThrLeuValValLeuHisArgAlaGlyAlaArgLeuAspVa
                                                                                 485 CCGACGCCGCCACTCTCACCCGACCCGTGCACGACGCTGCCCGGGGGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="IMAGE:2014405"
/clone_lib="NCI_CGAP_Brn23"
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                                                                                                                                                                                                                                         124 isArgAspValAlaGlyTyrLeuArgThrAlaThrGly 136
                                                                                                                                                                                                                                                                 335 ATCGCGATGTCGCACGGTACCTGCGCGCGCGCGGGG 298
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Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AI362049.1 GI:4113670
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;, mRNA sequence.
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4.866
                                                                                                                                                                                                                                                                                                                                seq_name: gb_est19:AI362049
                                                                                                                                                                                                                                                                                                                                                                                seq_documentation_block:
LOCUS AI362049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  human.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bonaldo, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. cDNA Sequencing by: Washington University Genome Sequencing Center DNA Sequencing by: Washington University Genome Sequencing Clone distribution: NCI-CGPP clone distribution information can be found through the I.M.AG.E. Consortium/LINL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 729 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 459.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AI198233 579 bp mRNA EST 02-DEC-1998 qi55d12.xl NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:1860407 3' similar to TR:Q16361 Q16361 CELL CYCLE NEGATIVE REGULATOR BETA FORM ;contains LTR9.b3 TAR1 TAR1 repetitive element ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    issue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 579)
NCI/MINDS-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index
Unpublished (1998)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
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/clone="Inb=NcIE:1860407"
/clone_lib=NcI_CGAP_Brn25"
/tissue_type="anaplastic oligodendroglioma"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57 rAlaArgValAlaGluLeuLeuLeuHisGlyAlaGluProAsnCysA 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            74 laAspProAlaThrLeuThrÀrgProValHisAspAlaAlaArgGluGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41 GlyValAsnArgPheGlyArgArgAlaIleGlnValMetMetGlySe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to: 579
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                                                                                                                     AI198233.1 GI:3750839
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US-09-016-869A-4 x AI198233/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            400.00
4.545
91.667
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Ratio:
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                                                                                                                                                                        human.
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source

FEATURES

BASE COUNT

ORIGIN

Sequencing Center information can be

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/note-"Organ: colon, vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site-1: Not I: Site-2: Eco RI; Plasmid DNA from the normalized library NCI_CGAP_COIO was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer. In a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (clonelDs 1057416-1061255, and 1144584-1145351).

Subtraction by Bento Soares and M. Fatima Bonaldo. " a 220 c 219 g 179 t lothers
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi,
Mammalia; Eutheria, Primates; Catarrhini, Hominidae, Homo.
1 (bases 1 to 614)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seg_documentation_block: 28-APR-1999
LOCUS AQ496105 614 bp DNA GSS 28-APR-1999
DEFINITION HS.5075_A1_F12_T7 RPCI-11 Human Male BAC Library Homo sapiens
genomic_clone Plate=651 Col-23 Row*K, genomic_survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      627 GCCCAGCGTTTAGGGCAGCAGCGCTTC.....CTAGAAGACCAGGTCA 584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   483 TGCCCGGGAGGGCTTCCTGGACACGCTGGTGGTGCTGCACCGGGCCGGGG 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53 etMetMetGlySerAlaArgValAlaGluLeuLeuLeuHisGlyAla 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70 GluProAsnCysAlaAspProAlaThrLeuThrArgProValHisAspAl 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38 pProAsn.....GlyValAsnArgPheGlyArgArgAlaIleGlnValM :||||:: |||||||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22 AlaArgGlyLeuValGluLysValArgHisSerTrpGluAlaGlyAlaAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         to: 774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length: 117
Gaps: 2
Percent Identity: 74.359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to reverse of: AI765096 from: 1
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CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

CORD. Library Requencing Context of the Context 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_documentation_block:

LOCUS AI755096

AI755096

DEFINITION W148D08.x1 NCI_CGAP_CG16 Homo sapiens CDNA clone IMAGE:2193463 3'

DEFINITION W148D08.x1 NCI_CGAP_CG16 Homo sapiens CDNA clone IMAGE:2193463 3'

SIMPLED TR:Q13399 Q13399 HYPOTHETICAL 18.1 KDA PROTEIN ; contains INTRY.b3 MER22 repetitive element ;, mRNA sequence.

ACCESSION AI765096.1 G1:5231605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla: Eutheria: Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 774)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Unpublished (1997)

On Feb 22, 1999 this sequence version replaced gi:4283180.
Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550

Email: Robert_Strausberg@nih.gov
Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100
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                                                                                                                                                                                                                                        51 GlnValMetMetGlySerAlaArgValAlaGluLeuLeuLeuLeuHi
                                                                                                                                                                            to: 580
       Percent Identity: 91.860
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/clone="iMAGE:2393463"
/clone=lib="NCI_CGAP_Co16"
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/lab_host="DH10B"
                                                                                                                                                                            from:
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                                                                                                                                                                         Align seg 1/1 to reverse of: AI362049
                                                                  alignment_block:
US-09-016-869A-4 x AI362049/rev
       95.349
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       134 laThrGly 136
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       Percent Similarity:
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ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
AUTHORS
TITLE
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KEYWORDS
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JOURNAL MEDLINE

COMMENT

TITLE

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CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

Www-bio.llnl.gov/bbrp/Amage/Amage.html

Insert Length: 872 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 394.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A1363262 708 bp mRNA EST 16-FEB-1999 95495f03.x NCI_CGARP_BRID31 Homo sapiens cDNA clone INAGE:2016029 3. similar to TR:013195 013195 P16INK4/AMTS1 [2] TR:Q13399 ;contains LTR9.b3 TAR1 repetitive element ;, mRNA sequence.
                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 708)
NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurological Siorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/PRGAR); Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41 GlyValAsnArgPheGlyArgArgAlaIleGlnValMetMetGlySe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   564 GGCAGCAGCCGCTTC.....CTAGAAGANCAGGTCATGATGATGCCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="InAGE:2016029"
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/tlssue_type="qlioblastoma (pooled)"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to: 708
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                                                                                                                                                                             AI363262.1 GI:4114883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_block:
US-09-016-869A-4 x A1363262/rev
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88.542
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                         seq_documentation_block:
LOCUS AI363262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    source
                                                                             DEFINITION
                                                                                                                                                                                                                                                      ORGANISM
                                                                                                                                                   ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                         REFERENCE
AUTHORS
TITLE
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ORIGIN
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                                                                                                                                                                                                    KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMMENT
                                                                                                                                                                                                                              SOURCE
                                                                             on Dec 15, 1999 this sequence version replaced gi:4575297.
Contact: Mahairas GG, Wallace JC, Hood L
Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
Oniversity of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3818
Fax: (206) 616-3818
Fax: (206) 616-3818
Fax: (206) 616-3818
Clones are derived from the human BAC library RPCI-11. For BAC
Library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
Seq Primer: 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anotes Mcstor: pBACe3.6; Site_1: ECORI; Site_2: ECORI;
Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of ECORI and ECORI Methylase. Size selected DNA was cloned into the pBACe3.6 vector and partially good 131 theres
  Sequence-tagged connectors: A sequence approach to mapping
scanning the human genome
Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
99380589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="Plate=651 col=23 Row=K"
/clone_lib="RPCI-11 Human Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84 isAspAlaAlaArgGluGlyPheLeuAspThrLeuValValLeuHisArg 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           101 AlaGlyAlaArgLeuAspValArgAspAlaTrpGlyArgLeuProValAs 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         441 GCCGGGCGCGCGCTGGACGTGCGTATGCCTGGGGCCGTCTGCCCGTGGA 490
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67 sGlyAlaGluProAsnCysAlaAspProAlaThrLeuThrArgProValH 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length: 86
Gaps: 0
Percent Identity: 89.535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to: AQ496105 from: 1 to: 614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo, sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      High quality sequence stop: 614. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Quality: 391.00
Ratio: 4.827
Percent Similarity: 94.186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_block:
US-09-016-869A-4 x AQ496105:
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BASE COUNT

FEATURES

521

57

117

2 others

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A1954684 563 bp mRNA EST 08-MAR-2000 wq34h12.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2473223 3' similar to SW:CDN2_HUMAN P42771 CYCLIN-DEPENDENT KINASE 4 INHIBITOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CRP clone distribution information can be
found through the I.M.A.G.E. Consortium/LiNL at:
www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(Dases 1 to 563)

NCI-GAP http://www.ncbi.nlm.nlh.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausbergenih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93 spthrLeuvalvalLeuHisArgAlaGlyAlaArgLeuAspValArgAsp 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    110 AlarrychyargLeuProValAspLeuAlaGluGluArgGlyHisArgAs 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    428 ACACGCTGGTGCTGCACCGGCCGGGCGCGCGCTGGACGTGCGCGAT 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    378 GCCTGGGGCCGTCTGCCCGTGGACCTGGCTGAGGAGCTGGGCCATCGCGA 329
                                                                                                                                                                                                                                                                           51 ......GlnValMetMetGlySerAlaArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      577 GCAGCAGCCGCTTCCTAGAAGACCAGGTCATGATGAT.GGCAGCGCCGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              478 CGCCACTCTCACCCGACCCGTGCACGCTGCCCGGGAGGGGTTCCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       76 oAlaThrLeuThrArgProValHisAspAlaAlaArgGluGlyPheLeuA
                                                                                                                                                                                                                                                                                                                                                                                            627 CCCGCNGCTGTGGCCCTCGTGCTGATGCTACTGAGAGCCCAGCGTCTAGG
                                                                                                                                                                                                                                          32 SerTrpGluAlaGlyAlaAspProAsnGlyVal...AsnArgPheGlyAr
                                                                                                                                                                                                                                                                                                                                            47 gArgAlaIle.....
                                                                                                                                                                                               to: 729
                                                    Gaps: 2
Percent Identity: 69.291
                                                                                                                                                                                               from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    126 pValAlaGlyTyrLeuArgThrAlaThrGly 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1 to reverse of: AI817709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; mRNA sequence.
A1954684
A1954684.1 GI:5746994
                                                                                                                      alignment_block:
US-09-016-869A-4 x AI817709/rev
                         384.00
3.959
76.378
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_documentation_block:
LOCUS A1954684
                                                                         Percent Similarity:
                                                    Ratio
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     alignment_scores:
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo. Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 729)

NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BRGAP), Tumor Gene Index. On Apr 7, 1998 this sequence version replaced gi:3035534. Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550

Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Donaldo, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.lnl.gov/Dbrp/Amage.html
Insert Length: 848 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 468.

Location/Qualifiers

1. 729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: Robert_Strausberg@nih.gov
Ilssue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_documentation_block:
LOCUS AI817709 729 bp mRNA EST 21-DEC-1999
DEFINITION Wk55c11.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2413364 3'
Similar to TR:Q13399 Q13399 HYPOTHETICAL 18.1 KDA PROTEIN ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
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                                                                                                                                                                                          5 others
74 laAspProAlaThrLeuThrArgProValHisAspAlaAlaArgGluGly
                         124 1sArgAspValAlaGlyTyrLeuArgThrAlaThrGly 136
                                                                                                                                                                                                                                                                                                                      143 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence.
AI817709
AI817709.1 GI:5436788
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                                                                                                                                                                                                                                                                                                                                                                                       seq_name: gb_est25:AI817709
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source

FEATURES

BASE COUNT ORIGIN

429

93

VERSION KEYWORDS SOURCE ORGANISM

ACCESSION

REFERENCE AUTHORS TITLE

JOURNAL COMMENT

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US-09-016-869A-4 x AI885362/rev
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5.027
97.403
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                                                                                                                                                                                                                                          Bonaldo, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality:
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ORIGIN
    AUTHORS
TITLE
                                                                                        JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURES
                                                                                                            COMMENT
                                                                                                                                                                                                                                 /note="Vector: pr773D-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library NCI_CGAP_GC4 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made ifform the same library (cloneIDs 1257096-1258631, 1469064-1470983, and 147592-1476743). Subtraction by Bento Soares and M. Fatima Bonaido. "subtraction by 158 c 169 g 124 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sed_documentation_block:

LOCUS AIRB5362 528 bp mRNA EST 07-MAR-2000

DEFINITION #192h4.x1 NCL_CGAP_Brn25 Homo sapiens CDNA clone IMAGE:2432407 3'

similar to SW:CDN2_HUMAN P42771 CYCLIN-DEPENDENT KINASE 4 INHIBITOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 528)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCCGACCCGTGCACGACGCTGCCCGGGAGGCTTCCTGGACACGCTGGTG 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97 ValLeuHisArgAlaGlyAlaArgLeuAspValArgAspAlaTrpGlyAr 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   80 hrargProvalHisAspAlaAlaArgGluGlyPheLeuAspThrLeuVal 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63 uLeuLeuLeuHisGlyAlaGluProAsnCysAlaAspProAlaThrLeuT
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/db_xref="taxon:9606"
/clone="InAcE:247323"
/clone_lib="NCI_CGAP_GC6"
/tissue_type="pooled germ cell tumors"
/lab_host="DH108"
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Gaps: 0
Percent Identity: 88.889
Insert Length: 613 Std Error: 0.00 Seq primer: -40UP from Gibco High quality sequence stop: 460. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A ;, mRNA sequence.
AI885362
AI885362.1 GI:5590526
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314 ACCTGCGCGCGGCTGCGGGG 295
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US-09-016-869A-4 x AI954684/rev
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4.590
92.222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality:
Ratio:
Percent Similarity:
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                                                                                        source
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KEYWORDS
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                                                                  FEATURES
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CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/Link at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 626 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 465.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
Mational Cancer Institute / National Institute of Neurological
Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/BTGAP), Tumor Gene Index
(Dipublished (1998)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausbergenih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D., Ph.D.
Ph.D.
CONA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="anaplastic oligodendroglioma"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          76 OAlaThrLeuThrArgProValHisAspAlaAlaArgGluGlyPheLeuA 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         110 AlaTrpGlyArgLeuProValAspLeuAlaGluGluArgGlyHisArgAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   478 CGCCACTCTCACCCGACCCGTGCACGACGCTGCCCGGGAGGGCTTCCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to reverse of: AI885362 from: 1 to: 528
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Percent Identity: 94.805
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            126 pValAlaGlyTyrLeuArgThrAlaThrGly 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   328 TGTCGCACGGTACCTGCGCGCGGCTGCGGGG 298
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SOURCE ORGANISM

REFERENCE AUTHORS TITLE

JOURNAL

ACCESSION VERSION KEYWORDS

DEFINITION

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CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.lln.in.gov/bbpt/image/image.html
Insert Length: 648 Std Error: 0.00
Seq primer: -400P from Gibco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AI638416 528 bp mRNA EST 14-DEC-1999 tt31903.x1 NOI_GCAB-GC6 Homo sapiens cDNA clone IMAGE:241410 3 % similar to TR:Q16361 Q16361 CELL CYCLE NEGATIVE REGULATOR BETA FORM ; contains LTR9.b3 TAR1 repetitive element ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo saplens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 528)
NCI-GAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI-GAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI-GAP http://www.ncbi.nlm.nih.gov/ncicgap.
Twational Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Unpublished (1997)
On Apr 7, 1998 this sequence version replaced g1:3036438.
Confact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
                                                                          AspalarrpGlyArgLeuProValAspLeuAlaGluGluArgGlyH1SAr 125
431 TGGACACGCTGGTGGTGCTGCACCGGGCCGGGGGCGCGGCTGGACGTGCGC 382
                                                                                                                                                    381 GATGCCTGGGGCCGTCTGCCCGTGGACCTGGCTGAGGAGCTGGGCCATCG 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="NCI_CGAP_GC6"
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Gaps: 0
Percent Identity: 92.308
                                                                                                                                                                                                                                           gAspValAlaGlyTyrLeuArgThrAlaThrGly 136
                                                                                                                                                                                                                                                                                 331 CGATGTCGCACGGTACCTGCGCGCGCGCGCGGGG 298
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Location/Qualifiers
1. .528
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US-09-016-869A-4 x A1638416/rev
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4.920
96.154
                                                                                                                                                                                                                                                                                                                                                                                            seq_name: gb_est23:A1638416
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LOCUS A1638416
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Ratio:
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ORIGIN
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KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS
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                                                                                                                                                                                                                                           125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausbergenth.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
CNA Glatribution: NGI-CGAP Clone distribution information can be found through the I.M.A.G.E. Consortium/LiNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 6.23 Std Error: 0.00
Seg primer: -40UP from Gibco
High quality sequence stop: 454.
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(Organism="Mono sapiens"

(Ab_xref="taxon:9606"

(Clone="Ith="taxon:9606"

(Clone="Ith="NCI_CGAP_GC6"

(Alsue_type="pooled germ cell tumors"

(Ab_host="Dooled germ ce
                                 AI633790 531 bp mRNA EST 14-DEC-1999 tt280e10.x1 NCI_CGAP_GC6 Homo sapiens CDNA clone IMAGE:2212122 3' similar to TR:016361 Q16361 CELL CYCLE NEGATIVE REGULATOR BETA FORM :contains LTR9.b3 TAR1 repetitive element ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                               Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 531)
NCI-CGAP http://www.ncbi.nlm.nlh.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       euaspThrLeuvalvalLeuHisArgAlaGlyAlaArgLeuAspValArg 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     75 pProAlaThrLeuThrArgProValHisAspAlaAlaArgGluGlyPheL 92
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4.973 Gaps: 0
96.154 Percent Identity: 93.590
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                                                                                                                                                                                                                               AI633790.1 GI:4685120
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US-09-016-869A-4 x AI633790/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tumor Gene Index
Unpublished (1997)
seq_documentation_block:
LOCUS A1633790
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Ratio:
Percent Similarity:
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source

FEATURES

alignment_scores

8

BASE COUNT

ORIGIN

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265 CGGGG 260
 alignment_scores:
                                                                                           alignment_block
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_documentation_block:
LOCUS AA909181 526 bp mRNA
DEFINITION 0112b04.51 Soarse_NFL_T_GBC_S1 Homo sapiens CDNA clone
IMAGE:1523215 3' similar to TR:016361 Q16361 CELL CYCLE NEGATIVE
REGULATOR BETA FORM ;, mRNA sequence.
                                                                                                                                                                                  AspAlaTrpGlyArgLeuProValAspLeuAlaGluGluArgGlyHisAr 125
                                                                       528 CGAGIGGCGGAGCIGCIGCIGCICCACGGCGCGGAGCCCAACIGCGNCGA 479
                                                                                                                               378 GATGCCTGGGGCCGTCTGCCCGTGGACCTGGCTGAGGAGCTGGGCCATCG 329
                                      75
                                                                                                              8
                                                                                                            75 pProAlaThrLeuThrArgProValHisAspAlaAlaArgGluGlyPheL
                                    59 ArgValAlaGluLeuLeuLeuLisGlyAlaGluProAsnCysAlaAs
to: 528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1523215"
/clone_lib="Soares_NFL_T_GBC_S1"
from: 1
                                                                                                                                                                                                                                                                                                                                                       128 CGATGTCGCACGGTACCTGCGCGCCGCCGGGG 295
                                                                                                                                                                                                                                                                                                                                     gAspValAlaGlyTyrLeuArgThrAlaThrGly 136
to reverse of: A1638416
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AA909181.1 GI:3048586
                                                                                                                                                                                                                                                                                                                                                                                                           seq_name: gb_estl3:AA909181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM
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AUTHORS
TITLE
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COMMENT
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465
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                                                                                                       68
                                                                                                                                                   84
                                                                                                                   68 lyAlaGluProAsnCysAlaAspProAlaThrLeuThrArgProValHis
                                                                                                      52 ValMetMetGlySerAlaArgValAlaGluLeuLeu.LeuLeuHisG
                                                                                 to: 526
Length: 86
Gaps: 1
Percent Identity: 88.372
                                                                                Align seg 1/1 to reverse of: AA909181 from: 1
                                                         US-09-016-869A-4 x AA909181/rev
         4.500
             Ratio:
                      Percent Similarity
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Run on:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
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Gapop 10.0 , Gapext 1.0
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Database

L76092 Mus musculu 880650 p161NK4a-CD 189920 Sequence 1 L76150 Mus musculu AF044336 Mus muscul AR062814 Sequence AR062815 Sequence AR062795 Sequence 25 U66087 Mus musculu U79631 Mus musculu L81167 Rattus norv U26727 Human hypot AR062785 Sequence AR001325 Sequence

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WERRPDRRA"
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AR062815 Sequence
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U60085 Mus musculu
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U59638 Mus musculu
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 AR037505 Sequence
I41159 Sequence 13
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AR037494 Sequence
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43. .552
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Mus musculus (clone: MARF) cDNA to mRNA.
Mus musculus
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MMU49281
MMU492815
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MMU79636
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MMU79639
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ARO10808
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases I to 713) Quelle, D. E., Zindy, F., Ashmun, R. A. and Sherr, C. J. Alternative reading frames of the INK4a tumor suppressor gene encode two unrelated proteins capable of inducing cell cycle a cell 83 (6), 993-1000 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 174807] from the original journal article. This sequence comes from Fig. 2.
                                                                    CICITCIGCICAACTACGGIGCAGAIGCGAACIGCGAGGACCCCACTACCITCICCCGCC 300
                                                                                                                                                                                                                                                                                                                    GCACGCCCAGGCCCTGGAACTTCGCGCCCAATCCCAAGAGCAGAGCTAAATCC-GCCTC 599
GGGCCGCCCACTCCAAGAGAGGGTTTTCTTGGTGAAGTTCGTGCGGATCCCGGAGACCCAG 120
                 AAGAGGCCGCACCGGAATCCTGGACCAGGTGATGATGATGGGGCAACGTTCACGTAGCAG 240
                                                                                                                                                                   CTCTTCTGCTCAACTACGGTGCAGATTCGAACTGCGAGGACCCCACTACCTTCTCCCGCC 323
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| GGAGTACAGCAGGGAGCATGGGTCGCAGGTTCTTGGTCACTGTAAGGATTCAGGGCGCGC
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                                                                              mammalian
                                                                                                                                                        78.9%; Score 672.8; DB 5;
llarity 99.6%; Pred. No. 6e-163;
Conservative 0; Mismatches 2;
                                                           1 (bases 1 to 713)
Sherr,C.J. and Quelle,D.E.
ARF-p19, a novel regulator of the m
Patent: US 572313.A 1 03-WAR-1998.
Location/Qualifiers
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/dranslation="MGRRFLVTVRIORAGRPLOERVFLVKFVRSRRPRTASCALAFVN
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                                                                                                                                                79.1%; Score 674.4; DB 12; Length 713;
Llarity 99.7%; Pred. No. 2.3e-163;
Conservative 0; Mismatches 1; Indels 1;
                          nd CDK6 cyclin D. comes from Fig.
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/gene="p16INK4a"
43. 552
/gene="p16INK4a"
/note="cDK4 and CDK6 c
This sequence comes fr
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/product="p16INK4a"
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                                                                                                                                                      Similarity
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/protein_id-"AAA85453.1"
/db_xref="G1:1162949"
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RLPLDLAAQERGHQDIVRYLRSAGCSLCSAGWSLCTAGNVAQTDGHSFSSSTPRALELR
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                                                                                               Eukaryota. Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria: Rodentia; Sciurognathi; Muridae; Murinae; Mus. I bases 1 to 840. Sciurognathi; Muridae; Mus. Quelle,D.E., Ashmun,R.A., Hannon,G.J., Rebberger,P.A., Trono,D., Richter,K.H., Walker,C., Beach,D., Sherr,C.J. and Serrano,M. Cloning and characterization of murine piginK4a and pisinK4b genes 0ncogene 11 (4), 635-645 (1995)
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MUSP16INK 846 bp mRNA ROD 20-JAN-1996
Mus musculus CDK4 and CDK6 inhibitor protein (p16ink4a) mRNA,
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                                                                                                                                                                                                                                                                                                                                            /codon_start=1
/function="CDK4 and CDK6 inhibitor; G1 phase
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Pred. No. 1.7e-154;
0; Mismatches 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     172
                                                                                                                                                                                                                           /organism="Mus musculus"
/db_xref="taxon:10090"
                                                            CDK4 inhibitor; CDK6 inhibitor.
Mus musculus cDNA to mRNA.
Mus musculus
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82. .585
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98.5%;
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Matches 646; Conservative
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/product-"cyclin dependent kinase inhibitor pl6INK4a"
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REPLDLIANYGADSNCEDPTTFSRPVHDAAREGFLDTLVVLHGSGARLDVRDAW
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 849)
Zhang,S., Ramsay,E.S. and Mock,B.A.
Cdkn2a, the cyclin-dependent kinase inhibitor encoding p16(INK4a)
and p19(ARK), is a candidate for the plasmacytoma susceptibility
locus, pctrl
Proc. Natl. Acad. Sci. U.S.A. 95 (5), 2429-2434 (1998)
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Zhang-X., Ramagay,E.S. and Mock,B.A.
Direct Submission
Submitted (23-JAN-1998) NCI/LG, NIH, 37 Convent Dr., Bethesda,
                                                                                                                                                                                                             196 GAATCCTGGACCAGGTGATGATGATGGCCAACGTTCACGTAGCAGCTCTTCTGCTCAACT 255
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AF044336.1 GI:3002948
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    /organism="Mus musculus"
/strain="DBA/2N"

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82. .588
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/product="gyclin dependent kinase inhibitor pl6inK4a"
/protein_id="aAcO8962.1"
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                                                                phosphorylation"
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                                                             /note="inefficient inhibitor/codon_start=1
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Sequence 44 from patent
AR062814
AR062814.1 GI:5990505
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82. SRR
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1. .849
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Medentia; Sclurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 849)
2 hang, S., Ramsay, E.S. and Mock, B.A.
Cdkn2a, the cyclin-dependent kinase inhibitor encoding p16(INK4a)
and p19(ARF), is a candidate for the plasmacytoma susceptibility
locus, pctr1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AF044335 849 bp mRNA ROD 01-APR-1998
Mus musculus strain BALB/CAnPt cyclin dependent kinase inhibitor
p161NK4a (CdKn2a) mRNA, complete cds.
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            315
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         GAGGGAGCGACCTGGACAGGAAAGGAATGGCATGAGAAACTGAGCGAAGGCGGCCGCGAA
                                                                                       CGCGGGAAGGCTTCCTGGACACGCTGGTGGTGCTGCACGGGTCAGGGGCTCGGCTGGATG
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                                                                                                                                                                  CCGCTGGGAACGTCGCCCAGACCGACGGCCATAGCTTCAGCTCAAGCACGCCCAGGGCCC
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Zhang, S., Ramsay, E.S. and Mock, B.A.
Direct Submission
Submitted (23-JAN-1998) NCI/LG, NIH,
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/organism="Mus musculus"
/strain="BALB/CADPt"
/db_xref="taxon:10090"
/tissue_type="spleen"
/chromosome="4"
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REFERENCE

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Probes for MTS1 gene and polynucleotides encoding mutant MTS1 genes Patent: US 5801236-A 25 01-SEP-1998;
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                                                                                                                                                                                                                                                                        TGTGGGGGATGCCTGGGGTGGCGCTGGACTTGGCCCAAGAGGGGGGACATCAAGA 433
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              134 GCTCTGGCTTTCGTGAACATGTTGTTGAGGCTAGAGAGGATCTTGAGAAGAGGGCCGCAC
                                                                   CGGAATCCTGGACCAGGTGATGATGATGGCCAACGTTCACGTAGCAGCTCTTCTGCTCAA
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44.0%; Score 375; DB 5; L.
Best Local Similarity 98.5%; Pred. No. 3.2e-86;
Matches 389; Conservative 0; Mismatches 5;
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Sequence 25 from patent US 5801236.
AR037515
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109 c 128 q
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Kamb, A.
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                                                                                                                                                                                                     Length 507;
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Pred. No. 3.2e-86;
0; Mismatches 5; Indels
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Pred. No. 4.6e-88;
0; Mismatches 8;
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Stone,S., Jlang,P. and Kamb,A.
Mouse MTSI gene
Patent: US 5843756-A 44 01-DEC-1998;
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Patent: US 5739027-A 25 14-AF
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Sequence 25 from patent
AR001335
AR001335.1 GI:3963402
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Best Local Similarity 98.5%;
Matches 389; Conservative C
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Matches 387; Conservative
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MMINK4A02 482 bp DNA ROD 02-JAN-1997
Mus musculus cyclin-dependent kinase inhibitor (pi6INK4a) gene,
exon 2 and partial cds.
U66087.
U66087.1 GI:1762922
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New York, NY 10016,
                                                                                                                                                                                  Length 395;
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         1 (bases 1 to 395)
Skolnick,M.H., Cannon-Albright,L.A. Germline mutations in the MTS gene Patent: US 5624819-A 25 29-APR-1997;
Location/Qualifiers
1. 395
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Submitted (05-AUG-1996) Pathology
Medical Center, 550 First Avenue,
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Malumbres, M. and Pellicer, A.
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Best Local Similarity 98.5%;
Matches 389; Conservative
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Mus musculus
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98.5%; Pred. No. 3.2e-86;
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Stone, S., Jiang, P. and Kamb, A.
Mouse MTSI gene
Patent: US 5843756-A 25 01-DEC-1998;
Location/Qualifiers
1. 395
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Sequence 25 from patent US 5624819.
I41169
I41169.1 GI:2001777
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                                                                                                                                                                                              5843756
                                                                      434 CATCGTGCGATATTTGCGTTCCGCTGGGTGCTCTT
                                                                                                                                                                                                                                                                                                                                                                                               /organism="unknown"
109 c 128 g
                                                                                                                                                                                 US.
                                                                                                                                                                            AR062795 395 bp
Sequence 25 from patent
AR062795
AR062795.1 GI:5990486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best_Local Similarity 98.5
Matches 389; Conservative
                                                                                                                                                                                                                                                                         Unknown.
Unclassified.
                                                                                                                                                                                                                                                                                                                                                                                                             73 a
                                                                                                                                                                                                                                                          Unknown.
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University USA

VERSION KEYWORDS SOURCE ORGANISM

DEFINITION ACCESSION

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RESULT 141169

314

254

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/product="cyclin-dependent kinase inhibitor protein"
/protein_id="AAD00236.1"
/d_xxef="fg1:4098166"
/translation="YWMMGNVHVAALLINVGADSNCEDPTFFSRPVHDAAREFLDTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MMU79632 339 bp DNA ROD 05-JAN-1999
Mus musculus cyclin-dependent kinase inhibitor protein (p16(INK4a))
gene, exon 2 and partial cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 339)
Santos, J., Melendez, B., Perez de Castro, I., Malumbres, M.,
Serrano, M., Pellicer, A. and Fernandez-Fiqueras, J.
Comparative analysis of the p16(INK4a) and p15(INK4b) DNA sequences
Direct Submission
Submitted (09-OCT-1996) Biologia, Universidad Autonoma de Madrid,
Cantoblanco, Madrid, Madrid 28049, Spain
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  270 AACTGCGAGGACCCCACTACCTTCTCCCGCCCGGTGCACGACGCAGGCGGGAAGGCTTC 329
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Pred. No. 6e-77;
                                                                                                                                                                        /map="between C3 and C6 bands"
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100.0%; Pred. No. c.
... 0; Mismatches
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                                                                                                 /organism="Mus spretus"
                                                                                                            /strain="SPRET/Ei"
/db_xref="taxon:10096"
/chromosome="4"
                                                                                                                                                                                                         /gene="p16(INK4a)"
1. 339
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                                                                                                                                                                                                                                 1. .339
/gene="p16(INK4a)"
                                                                                                                                                                                                                                                                                                          /gene="p16(INK4a)"
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Matches 339; Conservative
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VERSION
KEYWORDS
SOURCE
   TITLE
JOURNAL
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                                                                                                                                                                                        /product-"pl6INK4a"
/protein_id-"aAB39600.1"
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GRLPLDLAQERGHQDIVRYLRSAGCSLCSAGWSLCTAGNVAQTDGHSFSSSTP"
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Serrano,M., Pellicer,A. and Fernandez-Piqueras,J.
Comparative analysis of the p16(INK4a) and p15(INK4b) DNA sequences
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Mus spretus cyclin-dependent kinase inhibitor protein (pl6(INK4a))
                                                                                                                                                       /note="Allele: CDKN2; cyclin-dependent kinase inhibitor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAGGTGATGATGATGATGGGCAACGTTCACGTAGCAGCTCTTCTGCTCAACTACGGTGCAGAT 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        161 TCGAACTGCGAGGACCCCACTACCTTCTCCCGCCGGGTGCACGACGCAGCGCGGAAGGC 220
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 339)
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Santos,J., Melendez,B., Perez de Castro,I., Malumbres,M.,
Serrano,M., Pellicer,A. and Fernandez-Piqueras,J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 482;
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                                                                     join(U66086.1:94. .219,1. .444)
/gene="plGINK4a"
join(U66086.1:94. .219,104. .>444)
/gene="pl6INK4a"
                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
40.4%; Score 345; DB 12;
Best Local Similarity 100.0%; Pred. No. 1.8e-78;
Matches 345; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                               120
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/gene="p16INK4a"
                                          /chromosome="4"
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Unpublished
                                                                                                                                                                            /codon_start=1
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MSU79634
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KEYWORDS
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Search completed: July 21, 2000, 06:05:30 Job time: 14864 sec
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                     2 (bases 1 to 339)
Santos,J., Melendez,B., Perez de Castro,I., Malumbres,M.,
Santos,J., Melendez,B., and Fernandez-Piqueras,J.
Serrano,M., Pellicer,A. and Fernandez-Piqueras,J.
Submission
Submitted (09-OCT-1996) Biologia, Universidad Autonoma de Madrid,
Cantoblanco, Madrid, Madrid 28049, Spain
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 CTGGACACGCTGGTGCTGCAGGGGTCAGGGGCTCGGCTGGATGTGCGCGATGCCTGG 180
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTGGACACGCTGGTGCTGCACGGGTCAGGGGCTCGGCTGGATGTGCGCGATGCCTGG
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39.4%; Score 335.8; DB 12; Length 339;
Best Local Similarity 99.4%; Pred. No. 4e-76;
Matches 337; Conservative 0; Mismatches 2; Indels 0;
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                                                                                                                               1. .339
/organism="Mus musculus"
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/db_xref="taxon:10090"
/chromosome="4"
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                                                                                                                                                                                                                                     /gene="p16(INK4a)"
1. .339
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mouse inbred strains
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AUTHORS
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 339)
Santos, J., Melendez, B., Perez de Castro, I., Malumbres, M.,
Serrano, M., Pellicer, A. and Fernandez-Piqueras, J.
Comparative analysis of the p16(INK4a) and p15(INK4b) DNA sequences
In mouse inbred strains
Unpublished
2 (bases 1 to 339)
Santos, J., Melendez, B., Perez de Castro, I., Malumbres, M.,
Serrano, M., Pellicer, A. and Fernandez-Piqueras, J.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="cyclin-dependent kinase inhibitor protein"
/protein.id="AAD00230.1"
/db_xref="G1:4098154"
/translation="vaAMGNVHVAALLLNYGADSNCEDPTTFSRPVHDAAREGFLDTL
IVLHGSGARLDVRDAWGRLPLDLAQERGHQDIVNYLRSAGWSLCSAGWSLCTAGNVAQ
I DGHSFSSSTP"
111 g 73 t
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                                                                                                                                                                                                                                                                   Submitted (09-001-1996) Biologia, Universidad Autonoma de Madrid, Cantoblanco, Madrid, Madrid 28049, Spain Location/Qualifiers
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Pred. No. 4e-76;
0; Mismatches 2;
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/organism-"Mus musculus"
/strain-"Mus mus musculus"
/db_xref="taxon:10090"
/chromosome="4"
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/codon_start=1
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Best Local Similarity 99.4%;
Matches 337; Conservative
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Human p15(GS)p27 f CDK inhibitory fus Human p27-p16 fusi Multiple tumour su

Human p16p27 fu CDK inhibitory

Human MTS1 genomic Coding sequence 2 Human multiple tum Multiple tumour su Multiple tumour su Human multiple tum

Run on:

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01-MAR-1996 (first entry)
Cell-cycle regulatory protein p13.5 cDNA.
Cell-cycle regulatory protein p13.5; cyclin-dependent kinase inhibitor;
CCR; gene therapy; transgenic animal; cancer; cell proliferation;
Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 GGGCCGCCCACTCCAAGAGAGGGTTTTCTTGGTGAAGTTCGTGCGATCCCGGAGACCCAG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New cell cycle regulating proteins bind to cyclin dependent kinase and related nucleic acids, antibodies etc., used in diagnosis and therapy of abnormal cell proliferation, degeneration etc.

Example 4: Page 80; 109pp: Bnglish.

CDNA (T02965) coding for the mouse cell-cycle regulatory (CCR) protein plis (R82120) was isolated from an embryonal stem cell library using a probe based on human CCR pl6 cDNA (T02962).

The isolated CDNA can be used: to detect mutations in CCR genes that lead to cell proliferation; to breed transgenic annimals to study cellular disorders involving CCR allele mutation/misexpression; and to correct CCR-deficient cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GGAGTACAGCAGCGGGAGCATGGTCGAGGTTCTTGGTCACTGTAAGGATTCAGCGCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W09528483-A1.
26-CCT-1995.
14-APR-1995; U04636.
14-APR-1994; US-227371.
25-MXY-1994; US-248812.
14-SEP-1994; US-346511.
29-NOY-1994; US-346147.
(COLD-) COLD SPRING HARBOR LAB.
Beach DH, Demetrick DJ, Hannon GJ, Serrano M; WPI: 95-373798/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 851.4; DB 1;
Pred. No. 2.1e-234;
0; Mismatches 1;
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Best Local Similarity 99.9
Matches 852; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Description
                                                                                                                                                                                                                                         1 GGAGTACAGCAGCGGGAGCA.....GATACTTTTAAAATGTCAA
                                     Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                             hits satisfying chosen parameters:
                 GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
                                                                                                                                                                                                                                                                                                                                        311585 seqs, 125096042 residues
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Result No.

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                                                           cycle; cancer; diagnosis;
               AAGAGGGCCGCACCGGAATCCTGGACCAGGTGATGATGATGGGCAACGTTCACGTAGCAG
                                                                                                                                                                 GGGCTCGGCTGGATGTGCGCGATGCCTGGGGTCGCCTGCCGCTCGACTTGGCCCAAGAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                      601 CCCCGCCTTTTTCTTCTTAGCTTCACTTCTAGCGATGCTAGCGTGTCTAGCATGTGGCTT
Murine ARF-p19 cDNA.
ARF-p19; alternative reading frame; cell cycle; cancer; diagnos gene therapy; INK4a-p16; cyclin D-dependent kinase; CDK4; CDK6; inhibitor; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C-terminal fragment
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/product= ARF-p19
236. 613
/*tag= b
//product= INK4a-p16 C
1. 232
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/note= "Exon 1-beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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/note= "Exon 2"
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T62485;
16-AUG-1997 (first entry)
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drug screening

Claim 2; Fig 1: 49pp; English.

A murine cDNA molecule (162485) homologous to human INK4A beta

I ranscripts (see also 762486) was isolated from a mouse

transcripts (see also T62486) was isolated from a mouse

crythroleukaemia cell DNA library. Sequences of exon 1-beta are

spliced to exon 2 to create an open reading frame that encodes a

novel protein, ARP-19 (W1631), which induces cell cycle arrest
when overexpressed. Unrelated sequences from exon 1-alpha (not
shown) are spliced to the same exon 2 acceptor site to open another

reading frame that encodes INK41a-p16 (C-terminal fragment given in
W1632), an inhibitor of the cyclin D-dependent kinases CDK4 and

CDK6. Economical reutilisation of protein codding sequences in this
manner is without precedent in mammalian genomes and the unitary
inheritance of INK4a-p16 and ARF-p19 may reflect a dual requirement

Cor both proteins in cell cycle control. ARF-p19 nucleic acids can

be used as probes or primers, or in gene therapy protocols to

induce cell arrest in eukaryotes or (antisense) to inhibit ARF-p19

cancer. Human ARF-p19 cDNA (165486) has also been isolated.

Sequence 713 BP; 193 A; 195 C; 223 G; 162 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
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                                                                                                                                                                                                                                                                                                  Nucleic acid encoding ARF-p19 which induces cell cycle arrest when overexpressed - used for diagnosis and treatment of cancer, and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CGGTGCACGACGCGCGGGAAGGCTTCCTGGACACGCTGGTGGTGCTGCACGGGTCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24 GGAGTACAGCAGCGGGAGCATGGGTCGCAGGTTCTTGGTCATCGTGAGGATTCAGCGCGC
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Quelle DE, Sherr CJ;
WPI; 97-212919/19.
primer for
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Best Local Similarity 99.7
Matches 686; Conservative
  /note=
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25-SEP-1996; U15312.
27-SEP-1995; US-534975.
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WPI; 98-250421/22.

DNA specific for Multiple Tumour Suppressor IEI-beta gene - are useful for the diagnosis of cancers related to MTSIEI-beta useful for the diagnosis of cancers related to MTSIEI-beta mutation(s) and their treatment.

The useful for the diagnosis of cancers related to MTSIEI-beta mutation(s) and their treatment.

Sischosure: Figure 14; 72pp; English.

This is a mouse pi6 cDNA sequence used in the characterisation of the numan multiple tumour suppression proteins. MTSI, MST2 and MTSIEI-beta.

The MTS gene locus is also referred to as the familial melanoma (MLM) gene locus, located on human chromosome 9p21. Germ line mutations in MTS genes can be used in the diagnosis of predisposition to cancers, company and produced in the diagnosis of predisposition to cancers, Hyppoma, CLL, and cancers of the pancreas, breast, thyroid, covary, uterus, testis, kidney, stomach and rectum.

Sequence 395 BP; 73 A; 109 C; 128 G; 85 T;
                                                                                                                                                                                                                                                                                                                                          Mouse p16 cDNA fragment.
MTS1; WTS2; WTS1E1-beta; multiple tumour suppressor; diagnosis; cancer;
germ-line mutation; familial melanoma locus; MLM; predisposition; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 GCTCTGGCTTTCGTGAACATGTTGTTGATGAGAGGGATCTTGAGAAAAGAGGCCGCAC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              75 AAGAGGGTTTTCTTGGTGAAGTTCGTGCGATCCCGGAGACCCAGGACAGCG-AGCTGC 133
                                                                                                          134 GCTCTGGCTTTCGTGAACATGTTGTTGAGGCTAGAGGAGCGTTGAGAGAAGAGGGCCGCAC
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                    CTACGGTGCAGATTCGAACTGCGAGGACCCCACTACCTTCTCCGGGCGCGGTGCACGACGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 375; DB 1; Length 39
Pred. No. 3.7e-98;
0; Mismatches 5; Indels
                                                                                                                                                              590
                                                                                                                                                           556 TGGAACTTCGCGGCCAATCCCAAGAGCAGAGCTAA
                                                                                                                                                                                                473 IGGAACTICGCGGCCAAICCCAAGAGCAGAGCIAA
                                                                                                                                                                                                                                                                                                                                                                                             Mus sp. 185027-A. 14-APR-1998. 07-JUN-1995; 487033. 07-JUN-1995; 08-487033. 18-MAR-1994; US-214582. 18-MAR-1994; US-215086. 18-MAR-1994; US-215086. 14-APR-1994; US-215087. 17-MAR-1995; WO-U03316. (WYRI-) MYRIAD GENETICS INC.
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Best Local Similarity 98.5%;
Matches 389; Conservative
                                                                                                                                                                                                                                                                                        V11259 standard; cDNA; 395
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                                                                       GAATCCTGGACCAGGTGATGATGATGGCCAACGTTCACGTAGCAGCTCTTCTGCTCAACT
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TGCGCGATGCCTGGGGTCGCCTGCCGCTCGACTTGGCCCCAAGAGCGGGGACATCAAGACA
                                                    GCACGCCCAGGGCCCTGGAACTTCGCGGCCAATCCCAAGAGCAGAGCTAAATCC-GCCTC
                                                                                                                           AGCCCGCCTTTTTCTTCTTAGCTTCACTTCTAGCGATGCTAGCGTGTCTAGCATGTGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mouse multiple tumour suppressor gene segment - useful for primer
                                                                                                                                                                                                                                                                                                                                                         03-FEB-1999 (first entry)
Mouse multiple tumour suppressor 1 gene (MTS1) coding sequence.
Murine; multiple tumour suppressor 1 gene; MTS1; cancer; ss.
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The present sequence encodes mouse multiple tumour suppressor (MTS1) gene. The MTS1 gene can be used to design primers to detect abnormalities 1.e. polymorphisms which may predispose towards malignancies such as melanoma, leukaemia, astrocytoma, lymphoma, glioma, as well as tumours of e.g. the breast,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
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Pred. No. 3.6e-100;
0; Mismatches 8;
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86 A: 157 C;
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126..127
/*tag- b
/note- "splice site"
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/note- "splice site"
                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
1. .507
/*tag= a
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0
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98.0%;
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Jiang P, Kamb A, Stone S;
WPI; 99-044585/04.
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28-JUL-1995; US-508735.
07-JUN-1995; US-487033.
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Sequence 507 BP;
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Best Local Similarity
Matches 387; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This is the nucleotide sequence of a nucleic acid used in the michacure;

This is the nucleotide sequence of a nucleic acid used in the method of the invention involving the used of the multiple tumour suppressor (WTS) gene to diagnose and treat human cancers. The MTS gene is useful in the diagnosis and prognosis of human cancer, e.g. can by standard nucleic hybridisation techniques, of patient samples.

The mutated sequences are those that are present in somatic mutations of the gene in cancers. The vectors can be used for gene therapy contractions to replace function of mutated protein in patients. These can also be used to construct protein mimetics, also for therapeutic strategies. In addition the expression constructs can also be used to screen for drugs to be used for ancer therapy, and the protein citself may also be used to rescombinant MTS can be used to screen for drugs to be used for cancer therapy, and the protein itself may also be used to restore MTS function in a cell. Sequence 395 BP; 73 A; 109 C; 128 G; 85 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGCGCGCGAAGGCTTCCTGGACACGCTGGTGGTGCTGCACGGGTCAGGGGCTCGGCTGGA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAGAGGGTTTTCTTGGTGAAGTTCGTGCGATCCCGGAGACCCCAGGACAGCG-AGCTGC 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCTCTGGCTTTCGTGAACATGTTGTTGAGGCTAGAGAGGATCTTGAGAGAAGAGGCCGCAC 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 AAGAGGGGTTTTCTTGGTAAAGTTCGTGCGATCCCGGAGACCCAGGACAGCGTAGCTGC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acids based on multiple tumour suppressor, MTS, sequences useful as hybridisation probes, primers and recombinant production of MTS in the diagnosis and treatment of cancers related to MTS
                                                                                                                                                                                                                                                      04-DEC-1998 (first entry)
Nucleotide sequence of nucleic acid 6.
Multiple tumour suppressor; MTSLEIS; human; cancer; hybridisation; somatic mutation; gene therapy; ds.
                                                     CGGAATCCTGGACCAGGTGATGATGGGCCAACGTTCACGTAGCAGCTCTTCTGCTCAA
                                 TGTGCGCGATGCCTGGGGTCGCCTGCCGCTCGACTTGGCCCCAAGAGCGGGGGACATCAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 395;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44.0%; Score 375; DB 1; Length 39
98.5%; Pred. No. 3.7e-98;
ive 0; Mismatches 5; Indels
                                                                                                                      361 CATCGTGCGATATTTGCGTTCCGCTGGGTGCTCTT 395
                                                                                                     434 CATCGTGCGATATTTGCGTTCCGCTGGGTGCTCTT 468
                                                                                                                                                                                                                          BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MYRI-) MYRIAD GENETICS INC.
Kamb A;
WPI; 98-494842/42.
                                                                                                                                                                                                                          standard; DNA; 395
                                                                                                                                                                                                                                                                                                                        Homo saplens.
01-5801236-A.
01-582-1935, 480810.
07-JUN-1995; US-480810.
18-MAR-1994; US-214582.
18-MAR-1994; US-215087.
14-APR-1994; US-215087.
14-APR-1994; US-227369.
01-JUN-1994; US-227369.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 389; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
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Best Local S
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                                                                                                                                                                                                                                          V53840;
 241
                                 374
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                                                                                                                                                                                     RESULT
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The present sequence encodes murine multiple tumour suppressor IEI-beta (MTSIEI-beta) protein. Primers designed from the gene can be used to design primers to detect abnormalities i.e. polymorphisms which may predispose towards malignancies such as melanoma, leukaemia, astrocytoma, lymphoma, glioma, as well as tumours of e.g. the breast, thyroid, pancreas, uterus and kidneys.
                       241 AGCGCGCGAAGGCTTCCTGGACACGCTGGTGCTGCACGGGTCAGGGGCTCGGCTGGA 300
                                                                                          TGTGCGCGATGCCTGGGGTCGCCTGCCGCTCGACTTGGCCCAAGAGCGGGGACATCAAGA · 433
                                                                                                                  120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCTCTGGCTTTCGTGAACATGTTGTTGAGGCTAGAGGAGGATCTTGAGAAGAGGGCCGCAC 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGTGCGCGATGCCTGGGGTCGCCTGCCGCTCGACTTGGCCCAAGAGCGGGGAATCAAGA 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mouse multiple tumour suppressor gene segment – useful for primer
                                                                                                                                                                                                                                                                                                                                                                                  03-FEB-1999 (first entry)
CDNA encoding a murine multiple tumour suppressor IEI-beta p
Murine; multiple tumour suppressor 1 gene; MTS1; cancer; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 395;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 375; DB 1; Length by Pred. No. 3.7e-98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      85 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      128
                                                                                                                                                                                                            361 CATCGTGCGATATTTGCGTTCCGCTGGGTGCTCTT 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
44.0%; Score 375; DB
Best Local Similarity 98.5%; Pred. No. 3.7e
Matches 389; Conservative 0; Mismatches
                                                                                                                                                                                    CATCGTGCGATATTTGCGTTCCGCTGGGTGCTCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       design

Example 8; Fig 14; 80pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73 A;
                                                                                                                                                                                                                                                                                                                                            V70604 standard; cDNA; 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-DEC-1998.
28-UUL-1995; 058735.
28-UUL-1995; US-508735.
07-JUN-1995; US-487033.
(MYRI-) WYRRIAD-GENETICS II
Jiang P. Kamb A, Stone S;
WPI; 99-Q44585/Q4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Stone S;
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RESULT V70594

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standard; cDNA; 1131
                                                08-MAY-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 69.7
Matches 319; Conservative
                                                                                                                                                                                                                                                                                                                                  U03537.
US-214582.
US-215087.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 95-344626/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P-PSDB; R81700
                                                                                                                                                                                                                                                                            WO9525813-A1.
28-SEP-1995.
17-MAR-1995; U
                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 8; Fig 12A-B; 80pp; English.

Example 8; Fig 12A-B; 80pp; English.

The present sequence encodes a human multiple tumour suppressor IEI-beta fund The present protein. Primers designed from the gene can be used to design primers to detect abnormalities 1.e. polymorphisms which may predispose towards malignancies such as melanoma, leukaemia, astrocytoma, Imphoma, gilona, as well as tumours of e.g. the breast, thyroid, pancreas, uterus and kidneys.

Sequence 1131 BP; 337 C; 344 G; 229 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    251 CAGGGGCGCCCCCCTGTGGCCCTCGTGCTGATGCTACTGAGGAGCCAGCGTCTAGGGC 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  311 AGCAGCCGCTTCCTAGAAGACCAGGTCATGATGATGGCCAGCGCCCGAGTGGCGGAGCTG 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CGGCTGGATGTGCGCGATGCCTGGGGTCGCCTGCCGCTCGACTTGGCCCAAGAGCGGGGA 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cDNA encoding a human multiple tumour suppressor 1E1-beta protein.
Human; multiple tumour suppressor 1 gene; MTS1; cancer; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CGCACCGGAATCCT - - - GGACCAGGTGATGATGATGGGCAACGTTCACGTAGCAGCTCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CACGACGCAGCGCGGGAAGGCTTCCTGGACACGCTGGTGGTGCTGCTGCACGGGTCAGGGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mouse multiple tumour suppressor gene segment - useful for primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 226; DB 1; Length 1131;
Pred. No. 2.7e-55;
0; Mismatches 135; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     426 CATCAAGACATCGTGCGATATTTGCGTTCCGCTGGGTG 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualiflers
338. .655
/*tag= a
/product= MTSIE1-beta
                                                                             BP.
                                                                                                                                                                                                                                                                                                                                                          26.5%;
69.9%;
                                                                        V70594 standard; cDNA; 1131
                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 69.9 tes 320; Conservative
                                                                                                                                                                                                                                                                                                                               US5843756-A.
01-DEC-1998.
28-JUL-1995; 058735.
                                                                                                                                                                                                         Homo saptens
                                                                                                                      03-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Si
Matches 320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      σ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  311 AGCAGCCGCTTCCTAGAAGACCAGGTCATGATGATGGCCAGCGCCCGAGTGGCGGAGCTG 370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Detecting polymorphism associated with cancer precidisposition - also DNA, vectors and host cells e.g. for gene or protein replacement therapy and drug screening
Example 7; Pages 100-10; 148pp; English.

An individual can be diagnosed as having a predisposition to cancer by detecting an alteration in the wild type multiple tumour suppressor (MTS) gene, using gene probes which hybridise to the MTSIIbeta gene ORF T00744 (which encodes R81700); The above assay can also be used in the diagnosis and prognessis of melanoma, lymphoma, leukaemia and pancreas, breast and thyroid cancers, etc. sequence 1131 BP; 232 A; 327 C; 343 G; 229 T;
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Multiple tumour suppressor 1 exon 1 beta (MTS1Elbeta) gene ORF. Multiple tumour suppressor; MTS1Ebeta; cancer; diagnosis; assay; predisposition; melanoma; leukaemia; lymphoma; prognosis; pancreas; breast; thyroid; open reading frame; ORF; exon 1; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26.3%; Score 224.4; DB 1;
69.7%; Pred. No. 7.8e-55;
iive 0; Mismatches 136;
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338. .655
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18-MAR-1994; US-215087.
18-MAR-1994; US-215086.
14-APR-1994; US-215086.
01-UUN-1994; US-221938.
(WTAH.) UNIV UTAH RES FOUND.
Cannon-Albright LA, Kamb A,
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The CDNA sequences encoding several multiple tumour suppressor (MTS) polypeptides have been isolated and sequenced. This sequence encodes the MTS polypeptide MTSIE1-bera (R80947). MTS polypeptide-encoding CDNAs and mutants of these are useful for the diagnosis or prognosis of human cancer. Germ-line mutations of MTS CDNAs can be used for diagnosing predisposition to melanoma, leukaemia, astrocytoma, glioblastoma, lymphoma, glioma, Hodgkin's lymphoma, CLL and cancers of the pancreas, thyroid, ovary, uterus, testis, kidney, stomach and rectum. The wild type gene is useful for gene therapy and MTS polypeptides may also be used for protein replacement therapy. Also screening for potential cancer therapeutics.

Sequence 1131 BP: 232 A; 327 C; 343 G; 229 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CACTCCAAGAGAGGTTTTCTTGGTGAAGTTCGTGCGATCCCGGAGACCCAGGACAGCGA 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wild-type multiple tumour suppressor (MTS) gene and mutant sequences - useful in diagnosis, prognosis and therapy of human cancer, e.g. melanoma or leukaemia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-MAY-1996 (first entry)
Human MTS polypeptide, MTSIE1-beta encoding cDNA.
Multiple tumour suppressor; E1-alpha; diagnosis; cancer; leukaemia; astrocytoma; glioblastoma; Hodgkin's lymphoma; melanoma; glioma; gene therapy; chronic; ds.
Homo saplens.
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69.7%; Pred. No. 7.8e-55;
ive 0; Mismatches 136;
                                                                                                                                          /*tag= a
/product= MTS1E1-beta
                                                                                                                  Location/Qualifiers
338. .655
                                                                                                                                                                                                 18-MAR-1994; US-214581.
18-MAR-1994; US-214581.
18-MAR-1994; US-215086.
18-MAR-1994; US-215088.
18-MAR-1994; US-215087.
14-APR-1994; US-227369.
01-JUN-1994; US-227369.
(MYRL-) MYRIAD GENETICS INC.
Ramb A;
WPI: 95-344401/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 69.7
Matches 319; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human mutant multiple tumour suppressor gene sequences - for production of recombinant mutant polypeptide(s)
Disclosure; Columns 73-74; 72pp; English.
The present sequence the human multiple tumour suppressor gene (MTS1) Elbeta, useful in cancer diagnosis.
Sequence 1131 BP; 232 A; 327 C; 343 G; 229 T;
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Human multiple tumour suppressor gene 1 Elbeta.
Human; multiple; tumour; suppressor; MTS1; cancer; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26.3%; Score 224.4; DB 1; Length 69.7%; Pred. No. 7.8e-55; ive 0; Mismatches 136; Indels
                                                                                                                                                                                        426 CATCAAGACATCGTGCGATATTTGCGTTCCGCTGGGTG 463
                                                                                                                                                                                                                     Skolnick MH
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                                                                                                                                                                                                                                                                                                                                                     T69780 standard; cDNA; 1131
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/*tag= a
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14-APR-1994; US-227369.
00-JUN-1994; US-251938.
17-MAR-1995; WO-U03537.
07-JUN-1995; US-474177.
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Best Local Similarity
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P-PSDB; W19254.
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18-MAR-1994; U
14-APR-1994; U
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MTS1E1S. hybridisation;

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CACTCCAAGAGAGGGTTTTCTTGGTGAAGTTCGTGCGATCCCGGAGACCCCAGGACAGCGA 128
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Mottletc acids based on multiple tumour suppressor, MTS, sequences -
useful as hybridisation probes, primers and recombinant production
of MTS in the diagnosis and treatment of cancers related to MTS
                              CGGCTGGATGTGCGCGTGGCGTCGCCTGCCGCTCGACTTGGCCCAAGAGCGGGGA
                04-DEC-1998 (first entry)
Coding sequence 1 of the multiple tumour suppressor
Multiple tumour suppressor; MTSIEIS; human; cancer;
                                                                                                                                                                                                                               426 CATCAAGACATCGTGCGATATTTGCGTTCCGCTGGGTG 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= a
/product= "human MTS1E1S"
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18-MAR-1994; US-215086.
18-MAR-1994; US-215087.
14-APR-1994; US-227369.
01-JUN-1994; US-227369.
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US-480810.
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07-JUN-1995; 4
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V53830
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Claim 1: Fig 12; 72pp; English.

Claim 1: Fig 12; 72pp; English.

MTSIEI-beta. The MTS gene locus is also referred to as the familial melanoma (MLM) gene locus is also referred to step familial melanoma in MTS genes can be used in the diagnosis of predisposition to concers, e.g. melanoma, leukaemia, astrocytoma, gliboblastoma, lymphoma, glioma, Hodgkin's lymphoma, LiL, and cancers of the pancreas, breast, thyrold, ovary, uterus, testis, kidney, stomach and rectum.

Sequence 1131 BP; 232 A; 327 C; 343 G; 229 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                310
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                                                                                                                                                                                                                                                                          Human MTS1E1-beta cDNA.
MTS1E1-beta; multiple tumour suppressor; diagnosis; cancer;
germ-line mutation; familial melanoma locus; MLM; predisposition;
GCAGCGGGAGCATGGGTCGCAGGTTCTTGGTCACTGTAAGGATTCAGCGCGCGGGCCGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCTGCGCTCTGGCTTTCGTGAACATGTTGTTGAGGCTAGAGAGGATCTTGAGAAGAGGGC
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                                               CGGCTGGATGTGCGCGATGCCTGGGGTCGCCTGCCGCTCGACTTGGCCCCAAGAGCGGGGA
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/note= "multiple tumour suppressor"
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69.7%; Pred. No. 7.8e-55;
ive 0; Mismatches 136;
                                                                                                            426 CATCAAGACATCGTGCGATATTTGCGTTCCGCTGGGTG 463
                                                                                                                                Location/Qualifiers
338. .655
/*tag= a
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                                                                                                                                                                                                                         V11249 standard; cDNA; 1131
V11249;
                                                                                                                                                                                                                                                          15-JUL-1998 (first entry)
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Best Local Similarity 69.7
Matches 319; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-JUN-1995; 487033.
07-JUN-1995; US-487033.
18-MAR-1994; US-214582.
18-MAR-1994; US-215086.
18-MAR-1994; US-215087.
14-ARR-1994; US-227369.
01-JUN-1994; US-227369.
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                                                                                                                                                                                                                                                                                                                           Homo saplens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kamb A
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This is the nuclearies equence of the multiple tumour suppressor (MTSIEIS) gene, used in the method of the invention. The MTS gene is useful in the diagnosis and prognosis of human cancer, e.g. by standard nucleic hybridisation techniques, of patient samples. The mutated sequences are those that are present in somatic mutations of the gene in cancers. The vectors can be used for gene therapy strategies to replace function of mutated protein in patients. These can also be used to construct protein mimetics, also for therapeutic strategies. In addition the expression constructs can also be used for recombinant production of MTS. Recombinant MTS can be used to screen for drugs to be used for cancer therapy, and the protein stell may also be used to restore MTS function in a cell. Sequence 1131 BP; 232 A; 327 C; 343 G; 229 T; 131 GCGGCGAGAACATGGTGCGCAGGTTCATGGTGACCCTCCGGATTCGGCGCGCGTGCGGAC 190 Gaps 9 GCAGCGGGAGCATGGGTCGCAGGTTCTTGGTCACTGTAAGGATTCAGCGCGCGGGCCGCC ب ب Length 1131; Query Match 26.3%; Score 224.4; DB 1; Length 1 Best Local Similarity 69.7%; Pred. No. 7.8e-55; Matches 319; Conservative 0; Mismatches 136; Indels Column 73-76; 73pp; English.

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Query Match
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Claim 2; Fig 7; 49pp; English.

Claim 2; Fig 7; 49pp; English.

A human CDN molecule (T62486) corresponds to INK4A beta

transcripts and includes a reading frame coding for a novel protein

(W16323), designated ARF-p19, which induces cell cycle arrest when

coverexpressed. This reading frame asyntactically overlaps a second

reading frame that encodes INK4a-p16 (C-terminal region given in

W16324), an inhibitor of the cyclin D-dependent kinases CDK4 and

CDK6. Economical reutilisation of protein coding sequences in this

manner is without precedent in mammalian genomes and the unitary

inheritance of INK4a-p16 enammalian genomes and the unitary

choth proteins in cell cycle control. ARF-p19 nucleic acids can

be used as probes or primers, esp. for cancer diagnosis, or in gene

therapy protocols to induce cell arrest in eukaryotes or (antisense)

co inhibit ARF-p19 acidutty, and to create transgenic animals useful
                                                                                                                                                                                               191 CGCCGCGAGTGAGGGTTTTCGTGGTTCACATCCCGCGGGCTCACGGGGGGAGTGGGCAGCAC 250
                                                                                                                                                                                                                                                                                                                                                                     CACGACGCAGCGCGGGAAGGCTTCCTGGACACGCTGGTGGTGCTGCTGCACGGGTCAGGGGCT 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                               CGGCTGGATGTGCGCGATGCCTGGGGTCGCCTGCCGCTCGACTTGGCCCAAGAGGGGGGA 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ARF-p19; alternative reading frame; cell cycle; cancer; diagnosis; gene therapy; INK4a-p16; cyclin D-dependent kinase; CDK4; CDK6; inhibitor; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (SJUD-) ST JUDE CHILDREN'S RES HOSPITAL.

Quelle DE. Sherr CJ;

PHT: 97-212919/19.

P-PSDB: W16323-24.

Nucleic acid encoding ARF-p19 which induces cell cycle arrest when overexpressed - used for diagnosis and treatment of cancer, and for
                                                                                                  251 CAGGGGCCCCCCCCCCTCGTGCTACTACTGAGGAGCCAGCGTCTAGGGC
                                                                                                                                                                                                                                                                                              129 GCTGCGCTCTGGCTTTCGTGAACATGTTGTTGAGGCTAGAGGGATCTTGAGAAGAGGC
                                                                                                                                                                     189 CGCACCGGAATCCT---GGACCAGGTGATGATGGGCCAACGTTCACGTAGCAGCTCTT
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/*tag= a
/product= ARF-p19
338. .538
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T62486;
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Human ARF-p19 cDNA.
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25-SEP-1996; U15312.
27-SEP-1995; US-534975.
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T62486
AC T62486,
DT T62486,
DT T62486,
DF T6-AUG,
DW HINDIDIOS
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FT Cds
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                                                                                                             CACTCCAAGAGAGGGTTTTCTTGGTGAAGTTCGTGCGATCCCGGAGACCCCAGGACAGCGA 128
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                                                                                                                                                                                                                                                                               9 GCAGCGGGAGCATGGTCGCAGGTTCTTGGTCACTGTAAGGATTCAGCGCGGGGCCGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mouse multiple tumour suppressor gene segment – useful for primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mouse multiple tumour suppressor 2 gene (MTS2) coding sequence. Murine; multiple tumour suppressor 2 gene; MTS2; cancer; ss. Mus musculus.
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The present sequence encodes mouse multiple tumour suppressor (MTS2) gene. The MTS1 gene can be used to design primers to detect abnormalities i.e. polymorphisms which may predispose towards malignancies such as melanoma, leukaemia, astrocytoma, lymphoma, glioma, as well as tumours of e.g. the breast, thyroid, pancreas, uterus and kidneys.

Sequence 393 BP; 69 A; 124 C; 141 G; 59 T;
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                                             0; Mismatches 114; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               366 CGGCTGGATGTGCGCGATGCCTGGGGTCGCCTGCCGCTCGACTTGGC 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CGGCTGGACGTGCGGATGCCTGGGGCCGTCTGCCCGTGGACCTGGC
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    DB 1;
Score 208.6; DB 1
Pred. No. 1.9e-50;
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Jiang P. Kamb A, Stone S;
WPI; 99-044585/04.
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Best Local Similarity 77.8
Matches 196; Conservative
                                           290; Conservative
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28-JUL-1995; 058735.
28-JUL-1995; US-508735.
07-JUN-1995; US-487033.
                        Similarity
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P-PSDB; W70823
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                                                                                                                                                                                                                                              CTGGGGTCGCCTGCCGCTCGACTTGGCCCAAGAGCGGGGACATCAAGACATCGTGCGATA 445
                                                                                                                                                                                                                                                                                                                                                           Detecting polymorphism associated with cancer pre:disposition - also DNA, vectors and host cells e.g. for gene or protein replacement therapy and drug screening therapy and drug screening Example 8: Pages 91-92; 148pp; English.

An individual can be diagnosed as having a predisposition to cancer by detecting an alteration in the wild type multiple tumour suppressor (MTS) gene, using gene probes which hybridise to the MTSI gene ORF T00736 (which encodes R81701) mutant sequences T00749/50. The above assay can also be used in the diagnosis and prognosis of melanoma, lymphoma, leukaemia and pancreas, breast and thyroid
CCAGGTGATGATGATGGGCAACGTTCACGTAGCAGCTCTTCTGCTCAACTACGGTGCAGA 265
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Aultiple tumour suppressor 1 (MTS1) gene ORF.
Multiple tumour suppressor; MTS1; cancer; diagnosis; assay;
Multiple tumour suppressor; MTS1; cancer; diagnosis; assay;
predisposition; melanoma; leukaemia; lymphoma; prognosis;
pancreas; breast; thyroid; open reading frame; ORF; ds.
Homo sapiens.
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Pred. No. 2.4e-36;
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17-MAR-1995; U03537.
18-MAR-1994; US-214582.
18-MAR-1994; US-215087.
18-MAR-1994; US-215086.
14-APR-1994; US-215769.
01-JUN-1994; US-251938.
(MYRI-) MYRIAD GENETICS INC.
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P-PSDB; R81701.
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ilarity 74.6%;
Conservative
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Best Local Similarity
Matches 200; Conser
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APPLICANT: Beach, David H.
APPLICANT: Demetrick, Douglas J.
APPLICANT: Serrano, Manuel
APPLICANT: Serrano, Manuel
APPLICANT: Serrano, Gregory J.
TITLE OF INVENTION: Cell-cycle Regulatry Proteins, and Uses
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 853; DB 4; Length 853; Pred. No. 2.1e-239;
US-08-954-470-3

US-09-129-855A-3

US-08-474-177-1

US-08-478-177-1

US-08-480-810-1

US-08-188-251-1

US-09-120-130-1

US-09-120-130-1

US-09-120-130-1

US-09-120-130-1

US-09-120-130-1

US-08-480-810-36

US-08-480-810-36

US-08-480-810-36

US-08-480-810-36

US-08-480-810-36

US-08-480-810-36

US-08-480-810-36

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US-08-480-8110-36

US-08-848-811-36
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
PPULICATION NUMBER: US/08/306,511A
FTLING DATE: 14-SEP-194
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: CSI-001CP2
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 5:
SEDUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 5, Application US/08306511A
; Patent No. 5962316
; GENERAL INFORMATION:
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TYPE: nucleic acid
STRANDEDNESS: both
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Best Local Similarity
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US-08-306-511A-5
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US-08-306-511A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
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       July 21, 2000, 06:06:34; Search time 86.37 Seconds (without alignments) 1358.517 Million cell updates/sec
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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/5C_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/5D_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/COMB.seq:*
6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
7: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
7: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
                                    GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-486-047-13
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 1000000
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Perfect score:
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Result No.

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61 GGCCGCCCACTCCAAGAGAGGGTTTTCTTGGTGAAGTTCGTGCGATCCCGGAGACCCAG 120
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Pred. No. 2.1e-239;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REPERENCE/DOCKET NUMBER: MIV-071.09
TELECOMUNICATION INFORMATION:
TELEPHONE: (617) 832-1000
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 853 base pairs
                                                                                                                                                                      CORRATION TYPE: Floppy disk COMPUTER: IBM PC COMPALIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: ASCII(text) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/893,274 FILLIG DATE: 15-JULY-1997 CLASSIFICATION: 800 PRIOR APPLICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 18-NOVEMBER-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/991,997
FILING DATE: 17-DECEMBER-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-OCTOBER-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DETA:
APPLICATION NUMBER: US 08/248,812
FILING DATE: 25-WAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,371
FILING DATE: 14-APRIL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/154,915
                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/306,511
FILING DATE: 14-SEPTEMBER-1994
TITLE OF INVENTION: and Uses Rela
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSES: FOLEY, HOAG & ELIOT L.
STREET: ONE POST Office Square
CITY: Boston
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Matches 853; Conservative
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MOLECULE TYPE:
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; LOCATION:
US-08-893-274-5
                                                                                                                                                 COUNTRY:
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                                                                                               1 GGAGTACAGCAGCGGGGCATGGGTCGCAGGTTCTTGGTCACTGTAAGGATTCAGCGCGC
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                                      Indels
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                                     Mismatches
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APPLICANT: Demetrick, Douglas J.
APPLICANT: Serrano, Manuel
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                                     Matches 853; Conservative
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                                                                                                                                          GGGCTCGCCTCGGATGTGCGCGATGCCTGGGGTCGCCTGCCGCTCGACTTGGCCCAAGAGC
                                  CTCTTCTGCTCAACTACGGTGCAGATTCGAACTGCGAGGACCCCACTACCTTCTCCCGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Beach, David H.
APPLICANT: Demetrick, Douglas J.
APPLICANT: Demetrick, Douglas J.
APPLICANT: Serrano, Manuel
APPLICANT: Hannon, Call-Cycle Regulatory Proteins, and
TITLE OF INVENTION: Related Thereto
TUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley, Hoag & Eliot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: MA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordpad
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 5, Application US/08581918A Patent No. 6043030 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 02109
COMPUTER READABLE FORM:
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CTCTTCTGCTCAACTACGGTGCAGATTCGAACTGCGAGGACCCCACTACCTTCTCCCGGC

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Length 853,
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100.0%; Score 853; DB 5; 1
Best Local Similarity 100.0%; Pred. No. 2.1e-239;
Matches 853; Conservative 0; Mismatches 0;
              CLASSIFICATION: 435

CLASSIFICATION DATA:

APPLICATION NUMBER: US 08/497,214

FILING DATE: 30-UNN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/346,147

FILING DATE: 29-NOV-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/36,511

FILING DATE: 14-SEP-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/248,812

FILING DATE: 25-MAX-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/24,915

FILING DATE: 14-APR-1994

PRIOR APPLICATION NUMBER: US 08/227,371

FILING DATE: 14-APR-1994

PRIOR APPLICATION NUMBER: US 08/154,915

FILING DATE: 11-DEC-1993

PRIOR APPLICATION NUMBER: US 08/154,915

FILING DATE: 11-DEC-1993

ATTORNEY APPLICATION NUMBER: US 07/991,997

FILING DATE: 17-DEC-1992

ATTORNEY APPLICATION NUMBER: US 07/991,997

FILING DATE: 17-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Vincent, Matthew P.
REGISTRAINON NUMBER: 36,719
REFERENCE/DOCKET NUMBER: MIV-071.06
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (617) 812-1299
TELEFAX: (617) 812-1299
INFORMATION FOR SEO ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 853 base pairs
TYPE: nucleic acid
STRANDENESS: both
02-JAN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: CDS
LOCATION: 213..587
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US-08-581-918A-5
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CDS
213..587
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; LOCATION:
PCT-US95-04636-5
                                                  Query Match
Best Local
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                                                                                                           GCACGCCCAGGGCCCTGGAACTTCGCGGCCAATCCCCAAGAGCAGAGCTAAATCCGCCTCA
                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and TITLE OF INVENTION: Related Thereto NUMBER OF SEQUENCES: 10 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM C COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: ASCII(text)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:

APPLICATION WUMBER: US 08/346,147
FILING DATE: 29-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION WUMBER: US 08/306,511
FILING DATE: 14-5EP-1994
PRIOR APPLICATION NUMBER: US 08/248,812
FILING DATE: 25-MAY-1994
PROOR APPLICATION NUMBER: US 08/248,312
FILING DATE: 14-APR-1994
PRIOR APPLICATION NUMBER: US 08/227,371
FILING DATE: 14-APR-1994
FILING DATE: 14-APR-1994
FILING DATE: 14-APR-1994
FILING DATE: CAPACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: PCT/US95/04636
                                                                                                                                                                                                                                                                                                                                                                         Sequence 5, Application PC/TUS9504636 GENERAL INFORMATION:
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TYPE: nucleic acid
STRANDEDNESS: both
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CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                  841 TITAAAAIGICAA 853
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MOLECULE TYPE: CDNA
FEATURE:
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                             Gaps
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Length 853
                             0; Indels
100.0%; Score 853; DB 6; I
100.0%; Pred. No. 2.1e-239;
                             0; Mismatches
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US-08-534-975-1
; Sequence 1, Application US/08534975
                             Matches 853; Conservative
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GGGCTCGGCTGGATGTGCGCGATGCCTGGGGTCGCCTGCCGCTCGACTTGGCCCAAGAGC 420
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                                                                                                                                                                  GCACGCCCAGGGCCCTGGAACTTCGCGGCCAATCCCAAGAGCAGAGCTAAATCC-GCCTC
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Patent No. 587665

GENERAL INFORMATION:
APPLICANT: Sherr, Charles, J.
APPLICANT: Guelle, Dawn, E.
TITLE OF INVENTION: ARF-P19, A No. 5876965el Regulator of the TITLE OF INVENTION: Mammalian Cell Cycle
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ARESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C. STREET: 1100 New York Avenue Suite 600 CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: DATE: COMPATIBLE
COMPUTER: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/954,470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  684 TTAAAAAATACATAATAATGCTTTTTTT 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    660 TIAAAAATACATAATAATGCTTTTTT 687
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/534,975
FILING DATE: 28-SEP-1995
ATTORNEY AGENT IRFORMATION:
NAME: Fox, Samuel, L.
REGISTRATION NUMBER: 30,353
REFERENCE/DOCKET NUMBER: 0656.05'
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371.2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: DNA (genomic)
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: double
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LOCATION: 43...
FEATURE:
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US-08-954-470-1
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Patent No. 5723313
GENERAL INFORMATION:
APPLICANT: Sherr, Charles, J.
APPLICANT: Ouelle, Dawn, E.
TILLE OF INVENTION: ARF-p19, A No. 5723313e1 Regulator of the Mammalian Cell
TITLE OF INVENTION: Cycle
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Filopy disk
COMPUTER: IS FILOPY disk
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/534,975
FILING DATE: 28-5EP-1995
CLIASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 0656.0590000
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                            ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue Suite 600
STATE: Washington
STATE: Do. STATE: Do. STATE: Do. STATE: Do. STATE: Do. STATE: Do. STATE: STA
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TYPE: nucleic acid
STRANDEDNESS: double
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity
Matches 685; Conserv
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LOCATION: 43...
FEATURE:
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
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STRANDEDNESS:
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US-09-129-855A-1
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APPLICANT: Sherr, Charles, J.
APPLICANT: Quelle, Dawn, E.
TITLE OF INVENTION: ARF-p19, A No. 6046032el Regulator of the Mammalian TITLE OF INVENTION: Cell Cycle
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue Suie 600
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                                                                    78.9%; Score 672.8; DB 3; 99.6%; Pred. No. 6.2e-187; ive 0; Mismatches 2;
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Patent No. 6046032
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                                                                                 Best Local Similarity
Matches 685; Conserv
; NAME/KEY:
; LOCATION:
US-08-954-470-1
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US-09-129-855A-1
                                                                      Query Match
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ZIP: 20005
COMPUTER READABLE FORM:
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/129,855A
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Pred. No. 6.2e-187;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                   1340-1-023 CIP
                                                                                                                                                                           FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/954,470
FILING DATE: 20-0cT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/534,975
FILING DATE: 27-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 13
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: DNA (genomic) FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  78.9%;
99.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 713 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 99.6
Matches 685; Conservative
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AATGCTTTTTTTGCAATCACGGGAGGAGGAGGAGGAGCAGAAGGAGGAGGAGG 735
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   191 GTACCCCGATTCAGGTGATGATGATGGGCAACSTTCACGTAGCAGCTCTTCTGCTCAACT 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  796 GGGAATAATGGCTGGATTGTTTAAAAAATAAAATAAAGATACTTTTAAAATGTCAA 853
                                                                                                                                                                                                                   316 CGCGGGAAGGCTTCCTGGACACGCTGGTGCTGCACGGGTCAGGGGCTCGGCTGGATG
                                                                                                                                                                                                                                                                                           311 CGCGGGAAGGCTTCCTGGACACGCTGGTGGTGCTGCACGGGTCAGGGGCTCGGCTGGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          251 ACGGIGCAGATICGAACIGCGAGGACCCCACIACCTICICCCGCCCGGIGCACGACGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  496 CCGCTGGGAACGTCGCCCAGACGGGCATAGCTTCAGCTCAAGCACGCCCAGGGCCC
                                                                                                                                                                                                                                                                                                                                                                   376 TGCGCGATGCCTGGGGTCGCCTGCCGCTCGACTTGGCCCAAGAGGGGGGACATCAAGACA
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Patent No. 5843756
Patent No. 5843756
GENERAL INFORMATION:
SAPPLICANT: Stone, Steven
APPLICANT: Jiang, Ping
APPLICANT: Jiang, Ping
APPLICANT: Mamb, Alexander
TITLE OF INVENTION: MRS GENE AND THERAPEUTIC USE THEREOF
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
CITY: Washington
STRATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER: Eloppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US to be assigned
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-508-735-44
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                                                                                                                                                   196 GAATCCTGGACCAGGTGATGATGATGAGGCAACGTTCACGTAGCACCTCTTCTGCTCAACT 255
AGCCCGCCTTTTTCTTAGCTTCACTTCTAGCGATGCTAGCGTGTCTAGCATGTGGCT 659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 5, Application US/08627610
Patent No. 591997
GENERAL INFORMATION:
APPLICANT: Beach, David H.
APPLICANT: Beach, David H.
APPLICANT: Bepinho, Ronald A.
TITLE OF INVENTION: Transgenic Animals Having Modified Cell-Cycle
TITLE OF INVENTION: Regulation
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                         GGTGGTCTTTGTGTACCGCTGGGAACGTCGCCCAGACCGACGGGCATAGCTTCAGCTCAA
                                                                                                                                                                                                                                                         GCACGCCCAGGGCCCTGGAACTTCGCGGCCAATCCCAAGAGCAGAGCTAAATCC-GCCTC
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Pred. No. 6.5e-178;
0; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: ASCII(text)
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
PPLICATION NUMBER: US/08/627,610
FILING DATE: 04-APR-1996
CLASSIFICATION: 800
ATTONNEY, FAGENT INFORMATION:
NAME: VINCENT, MATCHEW P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTAAAAAATACATAATAATGCTTTTTT 687
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COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: USA
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Matches 648; Conservative
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75 AAGAGAGGTTTTCTTGGTGAAGTTCGTGCGATCCCGGAGACCCCAGGACAGCG-AGCTGC 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 GCTCTGGCTTTCGTGAACATGTTGTTGAGGCTAGAGAGGATCTTGAGAAGAGGCCGCGC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         194 CGGAATCCTGGACCAGGTGATGATGATGATGGGCAACGTTCACGTAGCAGCTCTTCTGCTCAA 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 AAGAGGGTTTTCTTGGTAAAGTTCGTGCGATCCCGGAGACCCAGGACAGCGTAGCTGC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 395;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5; Indels
                                                    ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,177
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
44.0%; Score 375; DB 1; I
Best Local Similarity 98.5%; Pred. No. 2.9e-100;
Matches 389; Conservative 0; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,369
FILING DATE: 14-APR-1994
PRIOR APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 24884-109348-E
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/03537
FILING DATE: 17-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,938
FILING DATE: 01-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-MAR-1994
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INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILLING CALL.
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08
FILING DATE: 18-MAR-1994
                                                                                                                                                     ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 395 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SEMET
                                                                    STREET: 1201 New CITY: Washington STATE: DC COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-474-177-25
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APPLICANT: SKOLNICK, Mark H.
APPLICANT: Cannon-Albright, Lisa A.
APPLICANT: Cannon-Albright, Lisa A.
APPLICANT: Ramb, Alexander
TITLE OF INVENTION: GERMLINE MUTATIONS IN THE MTS GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44.8%; Score 382.2; DB 3;
98.0%; Pred. No. 2.6e-102;
tive 0; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     556 TGGAACTTCGCGGCCAATCCCAAGAGCAGAGCTAA 590
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature;
CCATION: 467..468
US-08-508-735-44

NAME/KEY: misc_feature
'Splice site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
LOCATION: 126..127
OTHER INFORMATION: /note= "Splice site"
APPLICATION NUMBER: PCT/US95/03316
FILING DATE: 17-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Inhen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24884-109348
TELEPHONE: 202-962-4848
TELEPHONE: 202-962-4848
TELEPHONE: 202-962-4848
TELEPHONE: 202-962-4848
TELEPHONE: 202-962-8800
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS: LENGTH: 507 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
NOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ORGANISM: MUS MUS CULUS
PERMANISM: MUS MUS CULUS
                                                                                                                   24884-109348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 25, Application US/08474177 Patent No. 5624819
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Best Local Similarity 98.0°
Matches 387; Conservative
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US-08-474-177-25
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GENERAL INFORMATION:
APPLICANT: Kamb, Alexander
TITLE OF INVENTION:
NUMBER OF SQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEMP PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 08/08/487,033
FILING DATE: 07-UN-1995
CLASSTRICATION DATA:
APPLICATION NUMBER: PCT/US95/03316
FILING DATE: 17-WAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,938
FILING DATE: 01-UN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-WAR-1994
PRIOR APPLICATION NUMBER: US 08/215,086
FILING DATE: 18-WAR-1994
PRIOR APPLICATION NUMBER: US 08/214,582
FILING DATE: 14-APR-1994
PRIOR APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-WAR-1994
PRIOR APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-WAR-1994
ATPORTON NUMBER: US 08/214,582
FILING DATE: US 08/214,582
FILING DATE: US 08/214,582
FILING DATE: US 08/214,582
                                                                                                                                                                                                                    361 CATCGTGCGATATTTGCGTTCCGCTGGGTGCTCTT 395
                                                                                                                                                                                           434 CATCGIGCGATATITGCGITCCGCIGGGIGCTCTI 468
                                                                                                                                                                                                                                                                                                                                    US-08-487-033-25
; Sequence 25, Application US/08487033
; Patent No. 5739027
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INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 395 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: 11near
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-487-033-25
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                                                                                                                                                                                 61 GCTCTGGCTTTCGTGAACATGTTGTTGAGGCTAGAGGGATCTTGAGAAGAGGGCCGCAC 120
                                                                                                                                                                                                                                                                 314 AGCGCGGGAAGGCTTCCTGGACACGCTGGTGGTGCTGCACGGGTCAGGGGCTCGGCTGGA 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            301 TGTCCGCGATGCCTGGGGTCGCCTCCCGCTCGACTTCGCCCAAGAGCGGGGACATCAAGA 360
                                                                               75 AAGAGAGGGTTTTCTTGGTGAAGTTCGTGCGATCCCGGAGACCCAGGACAGCG-AGCTGC 133
                                                                                                                                                               134 GCTCTGGCTTTCGTGAACATGTTGTTGAGGCTAGAGGATCTTGAGAAGAGGCCGCGCC 193
                                                                                                                                                                                                                                            194 CGGAATCCTGGACCAGGTGATGATGATGGCCAACGTTCACGTAGCAGCTCTTCTGCTCAA 253
                                                                                                                                                                                                                                                                                                                            1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                              Length 395;
                                         Indels
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  Score 375; DB 2;
Pred. No. 2.9e-100;
0; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEDM PC compatible
OMPERATURE: IEDM PC compatible
OMPERATURE: Patentin Release #1.0, Vers
SOFTWARE: Patentin Release #1.0, Vers
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,810
FILING DATE: 07-JUN 1995
FILING DATE: 17-MAR-1995
PRIOR APPLICATION NUMBER: US 08/251,938
FILING DATE: 01-JUN 1994
PRIOR APPLICATION NUMBER: US 08/251,938
FILING DATE: 18-MAR.1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-MAR.1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,086
FILING DATE: 18-MAR.1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,086
FILING DATE: 18-MAR.1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,086
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,369
  44.0%;
98.5%;
Query Match
Best Local Similarity 98.5 Matches 389; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
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APPLICANT: Skolnick, Mark
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US-08-848-251-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  134 GCTCTGGCTTTCGTGAACATGTTGTTGAGGCTAGAGAGGATCTTGAGAAGAGGCCGCAC 193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 25, Application US/08508735
Patent No. 5843756
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Stone, Steven
APPLICANT: Kamb, Alexander
ITLE OF INVENTION: MTS GENE AND THERAPEUTIC USE THEREOF
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                          5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                          Score 375; DB 2; 1
Pred. No. 2.9e-100;
0; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CATCGIGCGATATITGCGITCCGCIGGGIGCICIT 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 14-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Inhen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24884-109348
TELEPAN: 202-962-8300
TELEFAX: 202-962-8300
                                                                                                                                                   INFORMATION FOR SEQ ID NO: 25: SEQUENCE CHARACTERISTICS: LENGTH: 395 base pairs TYPE: nucleic acid STANDEDNESS: double TOPOLOGY: linear MOLECULE TYPE: CDNA HYPOTHETIAL: NO
                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 98.5%;
Matches 389; Conservative
                                                                                                                                                                                                                                                                                              ; ANTI-SENSE: NO US-08-480-810-25
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US-08-508-735-25
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314 AGCGCGGGAAGGCTTCCTGGACACGCTGGTGCTGCACGGGTCAGGGGCTCGGCTGGA 373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               254 CTACGGTGCAGATTCGAACTGCGAGGACCCCACTACCTTCTCCCGCCGGGGGCACGACGC 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 AGCGCGCGAAGGCTTCCTGGACACGCTGGTGGTGCTGCACGGGTCAGGGGCTCGGCTGGA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        75 AAGAGAGGGTTTTCTTGGTGAAGTTCGTGCGATCCCGGAGACCCAGGACAGGG-AGCTGC 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        134 GCTCTGGCTTTCGTGAACATGTTGTTGAGGCTAGAGGATCTTGAGAAGAAGGCCCGCAC 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          194 CGGAATCCTGGACCAGGTGATGATGATGAGGCAACGTTCACGTAGCAGCTCTTCTGCTCAA 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 AAGAGGGGTTTTCTTGGTAAAGTTCGTGCGATCCCGGAGACCCAGGACAGCGTAGCTGC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 395;
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FO COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/508,735
FILING PATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match

44.0%; Score 375; DB 3; 1

Best Local Similarity 98.5%; Pred. No. 2.9e-100;

Matches 389; Conservative 0; Mismatches 5;
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PRIOR APPLICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US to be assigned
FILING DATE: 07-UN-1995

PRIOR APPLICATION NUMBER: US TO BAPLICATION NUMBER: PCT/US95/03316

FILING DATE: 17-MAR-1995

ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 248.957

REFERENCE/DOCKET NUMBER: 248.957

TELEFONOM: 202-962-83.00

INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 395 base pairs

TYPE: nucleic acid
STRANDENNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 25, Application US/08848251
Patent No. 5989815
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ANTI-SENSE: NO
US-08-508-735-25
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241 AGCGCGCGAAGGCTTCCTGGACACGCTGGTGCTGCACGGGTCAGGGGCTCGGCTGGA 300
    194 CGGAATCCTGGACCAGGTGATGATGATGGGCAACGTTCACGTAGCAGCTCTTCTGCTCAA 253
                                                                                   314 AGCGCGGGAAGGCTTCCTGGACACGCTGGTGCTGCTGCACGGGTCAGGGGCTCGGCTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Kamb, Alexander
TITLE OF INVENTION: MTS2 GENE
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IRM PC Compatible
SUSTANTE: DATE: 0.7-JUN 1995
CLASSIFICATION NUMBER: US/08/486,047
FILING DATE: 0.7-JUN 1995
READELCATION NUMBER: DET/US95/03316
FILING DATE: 17-MAR-1995
FRING APPLICATION DATA:
APPLICATION NUMBER: US 08/251,938
FILING DATE: 18-MAR-1994
PRIOR APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-MAR-1994
PRIOR APPLICATION NUMBER: US 08/215,086
FILING DATE: 18-MAR-1994
PRIOR APPLICATION NUMBER: US 08/217,369
FILING DATE: 14-APR-1994
PRIOR APPLICATION NUMBER: US 08/217,369
FILING DATE: 14-APR-1994
PRIOR APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-MAR-1994
PRIOR APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-MAR-1994
ATTORNEY/AGENT INPORMATION:
NAME: Therm Laffrey INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                     361 CATCGTGCGATATTTGCGTTCCGCTGGGTGCTCTT 395
                                                                                                                                                                                                                                                                                                                                               434 CATCGTGCGATATTTGCGTTCCGCTGGGTGCTCTT 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24884-109348-B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 25, Application US/08486047; Patent No. 5994095; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Ihnen, Jeffrey L. REGISTRATION NUMBER: 28,957 REFERENCE/DOCKET NUMBER: 24 TELECOMMUNICATION INFORMATION TELEPHONE: 202-962-4810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 395 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 15
US-08-486-047-25
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                                    TITLE OF INVENTION: GERMLINE MUTATIONS IN THE MTS GENE AND
TITLE OF INVENTION: METHOD FOR DETECTING PREDISPOSITION TO CANCER AT THE MTS
TITLE OF INVENTION: GENE
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ï
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 395;
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                                                                                                                                                                                                                                                       ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/848,251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 375; DB 4; I
Pred. No. 2.9e-100;
0; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/474,083
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/21,938
FILING DATE: 17-WAR-1995
PRIOR APPLICATION NUMBER: US 08/251,938
FILING DATE: 01-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-WAR-1994
PRIOR APPLICATION NUMBER: US 08/215,086
FILING DATE: 18-WAR-1994
PRIOR APPLICATION NUMBER: US 08/215,086
FILING DATE: 14-APR-1994
PRIOR APPLICATION NUMBER: US 08/215,086
FILING DATE: 14-APR-1994
APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-WAR-1994
ATTORNEY/AGENT INFORMATION:
FILING DATE: 18-WAR-1994
ATTORNEY/AGENT INFORMATION:
TELEPRONE: 202-962-4810
TELEFRONE: 202-962-8300
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 395 base pairs
TYPE: nucleic acid
TYPE: 11-no-1
Cannon-Albright, Lisa A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match
Best Local Similarity 98.5%;
Matches 389; Conservative
                      Kamb, Alexander
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                                                                                                                                                                                          CITY: Washington STATE: DC
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                                                                                                                                                                                                          134 GCTCTGGCTTTCGTGAACATGTTGTTGAGGCTAGAGAGGATCTTGAGAAGAGGGCCGCAC 193
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                                                                                                                                    1; Gaps
                                                                                                                                                                        181 CTACGGTGCAGATTCGAACTGCGAGGACCCCACTACCTTCTCCCGCCGGGTGCACGACGC
                                                                                                         Query Match

44.0%; Score 375; DB 4; Length 395;
Best Local Similarity 98.5%; Pred. No. 2.9e-100;
Matches 389; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: nucleic acid
; STRANDEDNES: double
; TOPOLOGY: linear
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-486-047-25
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Search completed: July 21, 2000, 06:06:41 Job time: 13807 sec

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                                 GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                              OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 1000000
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Perfect score:
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gb_gss14:*
gb_gss15:*
gb_gss16:*
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1118:
1120:
120:
121:
123:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

source BASE COUNT ORIGIN 899 156 809 FEATURES 8 ò g g δ ò AI817709 729 bp mRNA EST 21-DEC-1999 wk25c11.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2413364 3' similar to TR:Q13399 Q13399 HYPOTHETICAL 18.1 KDA PROTEIN ;, mRNA ALIGNMENTS RESULT 1 AI817709/C LOCUS DEFINITION

Bonaldo, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

CDNA Greguencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbpy/image/image.html
Insert Length: 848 Std Exror: 0.00

Seq primer: -400P from Gibco

High quality sequence stop: 468.

1. 729 T 3/]; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pI773 vector. Library is normalized, and was constructed by Bento Soares and M.Fatima Bonaldo." ï Email: Robert_Strausbergenih.gov Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D., Ph.D. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 729) 549 489 Neurological 96 AGTICGIGCGAICCCGGAGACCCAGGACAGCGGCTGCGCTCTGGCTTTCGTGAACATGT 155 ACATCCGCGNGCTCACGGGGAGTGGGGCAGCGCCAGGGGGCGCCCCCCGCNGCTGTGGCCCTCG 609 TGTTGAGGCTAGAGAGGATCTTGAGAAGAGGGCCGCACCGGAATCCTGGACCAGGTGATG 215 GCGAGGACCCCACTACCTTCTCCCGCCGGTGCACGCAGCGCGGGAAGGCTTCCTGG 333 728 TIGIGACCCTCCGNATICGGCGCGCGTCGGNCCCGCCGCGAGIGAGGGTTTTCGTGGTTC 669 216 ATGATG - GGCAACGTTCACGTAGCAGCTCTTCTGCTCAACTACGGTGCAGATTCGAACT 273 Gaps 36 TGSTCACTGTAAGGATTCAGCGCGGGGGGGCCGCCACAAGAGGGTTTTCTTGGTGA 95 CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima ACI/NIMDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurolog
Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/PITGAP), Tumor Gene Index
Unpublished (1998)
On Apr 7, 1998 this sequence version replaced gi:303534.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov 5 Query Match 21.9%; Score 187; DB 44; Length 729; Best Local Similarity 65.8%; Pred. No. 3.3e-41; Matches 283; Conservative 0; Mismatches 145; Indels /organism="Homo sapiens"
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217 530 277

LOCUS

AI363262/c

ORGANISM

REFERENCE AUTHORS TITLE

JOURNAL COMMENT

ACCESSION VERSION KEYWORDS SOURCE

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Homosapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

I (bases 1 to 648)

INIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.

National Institutes of Health, Mammalian Gene Collection (MGC)

AL Unpublished (1999)

On Apr 7, 1998 this sequence version replaced gi:3036295.

Contact: Robert Strausberg' Ph.D.

Tel: (301) 496-1550

Email: Robert Strausbergenih.gov

Tissue Procurement: ATCC

CONA Library Preparation: Edge BioSystems

CONA Library Preparation: Edge BioSystems

CONA Library Arrayed by: Trhe I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: NIH Intramural Sequencing Center (NISC)

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llni.gov/bbrp/image.html

Plate: LLCM0300 row: O column: 24

Seq primer: -21M13 forward primer (ABI).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       469 CGACCCGCCAACTCTCACCGGACCGTGCACGACGCTGCCCGGGAGGCCTTCCTGGACAC 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       398 GCCGCTCGACTTGGCCCAAGAGCGGGGACATCAAGACATCGTGCGATATTTGCGTTCCGC 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             349 GCCGGTGGACCTGGCTGAGGAGCTGGGCCATCGCGATGTCGCACGGTACCTGCGCGCGGC 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         278 GGACCCCACTACCTTCTCCCGCCCGGTGCACGCACGCGGGGAAGGCTTCCTGGACAC 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCTGGTGGTGCTGCACGGGTCAGGGGCTCGGCTGGATGTGCGCGATGCCTGGGGTCGCCT 397
                                      ACTGTAAGGATTCAGCGCGGGCCGCCCACTCCAAGAGAGGGTTTTCTTGGTGAAGTTC 100
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                                                                                                                                                                                                                                                                                                                                                                         649 CACAGGTCACNGGGGGAGTGGGCAGCGCAAGGGGCGCCCGCCGCTGTGGCTTCGTGCTG
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DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-GGAP clone distribution information can be
Gound through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 872 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stope: 394.
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9795f03.x1 NCI_CGAP_BEND3 Homo sapiens CDNA clone IMAGE:2016029 3/

similar to TR:013195 0103195 P16INK4/XMS1. [2] TR:013399; contains

LTR9, b3, TAR1 repetitive element; , mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo saplens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 708)
NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NAIJONAL Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/PRGAP), Tumor Gene Index
Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.
                                                                                                                  488 GCGCCGACNCCGCCACTCTCACCCGACCCGTGCACGACGCTGCCCGGGAGGGCTTCCTGG 429
                                                                                                                                                                                                                     394 GCCTGCCGCTCGACTTGGCCCAAGAGCGGGGACATCAAGACATCGTGCGATATTTGCGTT 453
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Bonaldo, Ph.D.
                                                                        ACACGCTGGTGGTGCTGCACGGGTCAGGGGCTCGGCTGGATGTGCGCGATGCCTGGGGTC
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67.1%; Pred. No. 1e-39;
tive 0; Mismatches 136; Indels 4;
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210 c 219 g 140 t
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AI363262.1 GI:4114883
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Best Local Similarity 67.1
Matches 286; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                   308 ceccreces 299
                                                                                                                                                                                                                                                                                                                                                              454 CCGCTGGGTG 463
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source

FEATURES

BASE COUNT

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And though the Lancer than the Lancer than the Lancer (1997)

On Feb 22, 1999, this sequence version replaced gi:4283180.

On Feb 22, 1999, this sequence version replaced gi:4283180.

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert Strausbergenih.gov

Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck,

M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

CLone distribution: NOI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/Link at:

www-bio.llnl.gov/bbrp/image/image.himl

Insert Length: 854 Std Error: 0.00

High quality sequence stop: 1000 seq primer: -400P from gibco

High quality sequence stop: 1000 seq primer: -1000 floatifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AI765096 774 bp mRNA EST 21-DEC-1999 4448D08.1 NCI_CGAP_CO16 Homo sapiens CDNA clone IMAGE:2393463 3' similar to TR:Q13399 Q13399 HYPOTHETICAL 18.1 KDA PROTEIN ; contains LTR9.b3 MER22 repetitive element ; mRNA sequence.
Directionally cloned into Ceul/Scel sites using the following 5' adaptor: taactataacggtcctaaggtagcga and 3' adaptor: tttcattacctcttctccgcaccccacataaa. Average insert size 900 bp. Library prepared by Edge BioSystems.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 774)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                     120 GGACAGCGAGCTGCGCTCTGGCTTTCGTGAACATGTTGTTGAGGGCTAGAGGGATCTTGA 179
                                                                                                                                                                                                                                                                                                                                                             GAAGAGGCCGCACCGGAATCCT---GGACCAGGTGATGATGATGGCCAACGTTCACGTA 236
                                                                                                                                                                                                                                                                                                                                                                                                                                              GCAGCTCTTCTGCTCAACTACGGTGCAGATTCGAACTGCGAGGACCCCACTACCTTCTCC 296
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                                                                                                                                                                                            Length 648;
                                                                                                                                                                                       Score 175.8; DB 71; Length
Pred. No. 4.1e-38;
0; Mismatches 97; Indels
                                                                                                           2 others
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AI765096.1 GI:5231605
                                                                                                                                                                                         tch 20.6%; al Similarity 71.2%; 247; Conservative
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Best Local S
Matches 247
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/note="Organ: colon; Vector: p1713D-pac (Pharmacia) with a modified polylinker; Site_1: Not 1; Site_2: Eco R1; Plasmid DnA from the normalized library NCL_GGAP_CO10 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs (cloneIDS 1057416-1061255, and 1144584-1145351).

subtraction by Bento Soares and M. Fatima Bonaldo. " a 220 c 221 g 179 t lothers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A1871381 590 bp mRNA EST 07-MAR-2000 w181d11.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2431317 3' similar to TR:Q16361 Q16361 CELL CYCLE NEGATIVE REGULATOR BETA FORM A1871381
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Budaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 590)
1 (CATANDS-GAPA PLETP://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                323 AGGCTTCCTGGACACGCTGGTGGTGCTGCACGGGTCAGGGGCTCGGCTGGATGTGCGCGA 382
                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 147 TGAACATGTTGTTGAGGCTAGAGAGGA-TCTTGAGAAGAGGGCCGCACCGGAATCCT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    534 GGAGCCCAATTGGGCCGACCCGCCACTTTCACCCGAACCGTGCACGACGCTGCCCGGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      383 TGCCTGGGGTCGCCTGCCGCTCGACTTGGCCCAAGAGCGGGGACATCAAGACATCGTGCG
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6
                                                                                                                                                                                                                                                                                                                                                                                                        Length 774;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                     19.4%; Score 165.6; DB 44;
llarity 66.9%; Pred. No. 2.8e-35;
Conservative 0; Mismatches 140; 1
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2393463"
/tissue_lib="NCI_CGAP_Col6"
/tissue_type="colon tumor, RER+"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     443 ATAITIGCGIICCGCIGGGIG 463
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Best Local Similarity
Matches 295; Conserv
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VERSION
KEYWORDS
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JOURNAL

COMMENT

source

FEATURES

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CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CRAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

Www-bio.llnl.gov/bbrp//lmage/hmil

Insert Length: 819 Std Error: 0.00

Seq primer: -40UP from Gibco

Seq primer: -40UP from Gibco

High quality sequence stop: 474.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T 3'); double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT/T3 vector. Library is normalized, and was constructed by Bento Soares and M-Ethima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1998)
On May 18, 1998 this sequence version replaced gi:3136859.
On fay 18, 1998 this sequence version replaced gi:3136859.
Contact: Robert Strausberg, Ph.D.
Email: Robert_Strausberg@nlh.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
                                          Chordata; Craniata; Vertebrata; Euteleostomi;
Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                379
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                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostor Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 579)
NCI/NINDS-CGAP http://www.ncbi.nlm.nlh.gov/ncicgap.
National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BEGAP), Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           264 GATTCGAACTGCGAGGACCCCACTACCTTCTCCCGCTGCGTGCACGACGCGGGGGAA 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               204 GACCAGGTGATGATGATGGCAACGTTCACGTAGCAGCTCTTCTGCTCAACTACGGTGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     384 GCCTGGGGTCGCCTGCCGCTCGACTTGGCCCAAGAGCGGGGACATCAAGACATCGTGCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         324 GCCTTCCTGGACACGCTGGTGGTGCTGCACGGGTCAGGGGCTCGGCTGGATGTGCGCGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism-"Homo sapiens"
/db_xref="taxon:9606"
/clone="IbARGE:2430933"
/clone=lib="NCI_CGAP_Brn25"
/tissue_type="anaplastic oligodendroglioma"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
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Pred. No. 4.2e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        444 TATTTGCGTTCCGCTGGGTG 463
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Best Local Similarity 75.4%;
Matches 196; Conservative
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                         Homo sapiens
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                   ORGANISM
                                                                                                     AUTHORS
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                                                                                REFERENCE
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                                                                                                                                                                                                                                                                          AIB70879 579 bp mRNA EST 07-MAR-2000 w177d11.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2430933 3' similar to TR:016361 016361 CELL CYCLE NEGATIVE REGULATOR BETA FORM 7, mRNA sequence.
AIB70879 AIR70879.1 GI:5544847
                                                                                                                                                                                                CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
              Unpublished (1998)
On Oct 30, 1998 this sequence version replaced gi:3813427.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                526 TGCTGCTCCACGGCGCGGAGCCCAACTGCGCCGACCCCGCCACTCTCACCCGACCCGTGC 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           367 GGCTGGATGTGCGCGATGCCTGGGGTCGCCTGCCGCTCGACTTGGCCCAAGAGCGGGGAC 426
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Bonaldo, Ph.D.
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Pred. No. 8.1e-34;
0; Mismatches 73
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ilarity 73.6%;
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Best Local 8
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BASE COUNT ORIGIN

Matches

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307

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406

346

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RESULT

LOCUS RESULT 6 A1870879/c

ACCESSION VERSION KEYWORDS

30-MAR-1999

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Information cancer institute, cancer benome Anatomy Froject (CGAP), Tumor Gene Index

Unpublished (1997)

Conteact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert_Strausberg@ih.gov

Tissue Procurement: Ash Alizadeh, John Byrd, M.D., Mike Grever,

M.D., Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LiNL at:

Www-bio.llnl.gov/bbrp/image.html

Insert Length: 755 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 457.

Location/Qualifiers

Lroe
                                                                                                                                                                                      tg13g05.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2108696 3' similar to SW:CDN2_HUMAN P42771 CYCLIN-DEPENDENT KINASE 4 INHIBITOR A ; contains LTR9.b3 TAR1 repetitive element ;, mRNA sequence. A1394605.1 GI:4224152
                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 566)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                       mRNA
                                             319 TACCTGCGCGCGGCTGCGGG 300
                                                                                                                                                                       266 bp
                       444 TATTIGCGTICCGCIGGGIG
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AI362049 AI362049 AI362049.1 GI:4113670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:

www.blo.lnl.gov/bbrp/lange/finage.html
Insert Length: 884 Std Error: 0.00
Seq primer: -400P from Gibco
High quality sequence stop: 321.
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1 (bases 1 to 580)

NGI/NINDS-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NGI/NINDS-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NGI/NINDS-GGAP institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index
Unpublished (1998)

Contact: Robert Strausberg, Ph.D.
Tel: (301) 486-1550

Fel: (301) 486-1550

Fenall: Robert_Strausberg@nlh.gov
                                                                                                                                                                                                                                                                                                                                                                                                                      Email: Robert_Strausberg@nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
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/clone="twaxon:9606"
/clone="twaxon:0406"
/clone=lib="NCI_CGAP_Brn23"
/tissue_type="qlioblastoma (pooled)"
/lab_host="DH100"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bonaldo, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D.
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Pred. No. 4.2e-33;
0; Mismatches 64,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
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75.4%;
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                                                                                                                                                                                                                                                                                                          /organism="Romo sapiens"
/db_xref="taxon:9606"
/clone="TAMGE:2108656"
/clone=lib="NCI_GGAP_CLL1"
/tisuse_type="B-cell, chronic lymphotic leukemia"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                             316 CGCGGGAAGGCTTCCTGGACACGCTGGTGGTGCTGCACGGGTCAGGGGCTCGGCTGGATG
                                                                                                                                                                                                                                             DB 39; Length 566;
                                                                                                                                                                                                                                          18.4%; Score 156.6; DB 73.9%; Pred. No. 8e-33; tive 0; Mismatches
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443

376

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요 à g RESULT 9 A1198233/c

LOCUS

VERSION KEYWORDS SOURCE ORGANISM

ACCESSION

JOURNAL COMMENT

REFERENCE AUTHORS TITLE

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/note="Vector: pBACe3.6; Site_1: ECORI; Site_2: ECORI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of ECORI and partially digested with a combination of ECORI and ECORI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at ECORI sites 11 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mahairas, G.G., Waliace, J.C., Smith, K., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: (206) 616-3618
The according for the control of the control o
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 614)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
                                                                       264 GATTCGAACTGCGAGGACCCCACTACCTTCTCCGGCCGGGTGCACGAGCGCGGGGAA 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AQ496105 614 bp DNA GSS 28-APR-1999 HS_5075_A1_F12_T7 RPC1-11 Human Male BAC Library Homo sapiens genomic clone Plate=651 Col=23 Row-K, genomic survey sequence. AQ496105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence-tagged connectors: A sequence approach to mapping scanning the human genome Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999) 99380589
                                                                                                                                                                                                                                         384 GCCTGGGGTCGCCTGCCGCTCGACTTGGCCCAAGAGCGGGGACATCAAGACATCGTGCGA
                                                                                                                                                                            GGCTTCCTGGACACGCTGGTGCTGCACGGGTCAGGGGCTCGGCTGGATGTGCGCGGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="Plate=651 Col=23 Row=K"
/clone_lib="RPCI-11 Human Male BAC Library"
/sex="male"
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/db_xref="taxon:9606"
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COMMENT
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CDNA Library Arrayed by: Greg Lennon, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

WWW-blo.lini.gov/Dbrp/image/image.html

Insert Length: 729 Std Error: 0.00

Seq primer: -400P from Gibco

High quality sequence stop: 459.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                              AI198233 579 bp mRNA EST 02-DEC-1998 4155012.x1 NCI_GCAP_BEN25 Homo sapiens cDNA clone IMAGE:1860407 3/ similar to TR:016361 0216361 CELL CYCLE NEGATIVE REGULATOR BETA FORM ;contains LTR9.b3 TAR1 TAR1 repetitive element ;, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: Robert_Strausberg@nih.gov
Ilssue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutherla; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 579)
NCI/NINDS-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI/NINDS-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI/NINDS-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index
Unpublished (1998)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
                                                                                                           TGCGCGATGCCTGGGGTCGCCTGCCGCTCGACTTGGCCCAAGAGCGGGACATCAAGACA 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Pred. No. 6.1e-32;
0; Mismatches 67; Indels 0;
                                                                                                                                                                                                                                                436 TCGTGCGATATTTGCGTTCCGCTGGGTG 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AI198233.1 GI:3750839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18.0%;
74.2%;
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source

FEATURES

ORIGIN

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204 GACCAGGTGATGATGATGGGCAACGTTCACGTAGCAGCTCTTCTGCTCAACTACGGTGCA 263

COUNT

BASE CO ORIGIN

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Conservative
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Best Local Simi
Matches 191;
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AUTHORS
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CDNA Library Arrayed by: Greg Lennon, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

CDNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: WCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llni.gov/Dbrp/lmage/image.html

Insert Length: 613 Std Error: 0.00

Seq primer: -400P from Gibco

High quality sequence stop: 460.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A1954684 563 bp mRNA EST 08-MAR-2000 wq34h12.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2473223 3' similar to SW:CDN2_HUMAN P42771 CYCLIN-DEPENDENT KINASE 4 INHIBITOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutherla; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 563)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NCI-CGAP institute, Cancer Genome Anatomy Project (CGAP), Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
mail: Robert_Strausberg@nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                   TICCTGGACACGCTGGTGGTGCTGCACGGGTCAGGGGCTCGGCTGGATGTGCGCGATGCC 386
                                                                                                                                                                                                                                                                                                                                               TGGGGTCGCCTGCCGCTCGACTTGGCCCAAGAGCGGGGACATCAAGACATCGTGCGATAT 446
                                                                                    207 CAGGIGAIGAIGAIGGGCAACGITCACGIAGCAGCICTICIGCICAACIACGGIGCAGAI 266
                                              Gaps
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                                                                                                                                                                        267 TCGAACTGCGAGGACCCCACTACCTTCTCCCGCCCGGTGCACGACGCAGCGCGGGAAGGC
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    Length
                                            68; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="INAGE:2473223"
/clone_lib="NCI_CGAP_GC6"
/tissue_type="pooled germ cell tumors"
/lab_host="DH108"
    DB 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA Library Preparation: M. Bento Soares,
Score 148.2; DB 1
Pred. No. 1.7e-30;
                                          0; Mismatches
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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  17.4%;
73.5%;
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A1954684
Query Match 17.4
Best Local Similarity 73.5
Matches 189; Conservative
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ACCESSION VERSION KEYWORDS SOURCE JOURNAL

FEATURES

REFERENCE

TITLE

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COUNT Library Arrayed by: Greg Lennon, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
NWW-blo.llni.gov/Dbrp/inage/image.html
Insert Length: 626 Std Error: 0.00
Seq primer: -400P from Gibco
High quality sequence stop: 465.
Location/Qualifiers
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Thel: (301) 496-1550
Email: Robert Strausbergenih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (bases 1 to 528)

NCI/NINDS-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NCI/NINDS-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.

Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           209 GGTGATGATGATGGGCAACGTTCACGTAGCAGCTCTTCTGCTCAACTACGGTGCAGATTC 268
                                                                                                                                                                                                                                                                                                                                                          269 GAACTGCGAGGACCCCACTACCTTCTCCCGCCGGTGCACGACGCAGGCGGGGAAGGCTT 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               489 CAACTG-GCCGACCCGCCAACTCTCACCCGACCCGTGCACGACGCTGCCCGGGAGGGCTT 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCTGGACACGCTGGTGGTGCTGCACGGGTCAGGGGCTCGGCTGGATGTGCGCGATGCCTG 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       389 GGGTCGCCTGCCGCTCGACTTGGCCCAAGAGCGGGGACATCAAGACATCGTGCGATATTT 448
                                                                                                                                                                                                                                                                 Gaps
1469064-1470983, and 1475592-1476743). Subtraction
Bento Soares and M. Fatima Bonaldo. "
158 c 169 g 124 t
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                                                                                                                                                                                               DB 46; Length 563;
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/clone_lib="NCI_CGAP_Brn25"
/tissue_type="anaplastic oligodendroglioma"
/lab_host="DH10B"
                                                                                                                                                                                     16.7%; Score 142.2; DB 4
74.9%; Pred. No. 7.6e-29;
tive 0; Mismatches 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1. .528
/organism="Homo sapiens"
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A1885362
A1885362.1 GI:5590526
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 528)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

Unpublished (1997)

On Apr 7, 1998 this sequence version replaced gi:3036438.

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert_Strausbergenih.gov

Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-GGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 648 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 462.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AIG38416 528 bp mRNA EST 14-DEC-1999 tt31903.xl NCI_CGAP_GC6 Homo sapiens CDNA Clone IMAGE:2242420 3' similar to TR:Q16361 Q16361 CELL CYCLE NEGATIVE REGULATOR BETA FORM AIG38416
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                                                                                                                                                                                                                                                                                                                                             234 GTAGCAGCTCTTCTGCTCAACTACGGTGCAGATTCGAACTGCGAGGACCCCACTACCTTC 293
                                                                                                                                                                                                                                                                                                                                                                  294 TCCCGCCCGGTGCACGACGCAGCGGGGAAGGCTTCCTGGACACGCTGGTGGTGCTGCAC 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                354 GGGTCAGGGGCTCGGCTGGATGTGCGCGATGCCTGGGGTCGCCTGCCGCTCGACTTGGCC 413
                                                                                                                                                                                                                                                                                                        Gaps
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cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             408 CGGGCCGGGGCGCGGGCTGGACGTGCGGATGCCTGGGGCCGTCTGCCCGTGGACCTGGCT
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                                                                                                                                                                                                                                                               Score 140.4; DB 45; Length 528; Pred. No. 2.4e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    414 CAAGAGCGGGACATCAAGACATCGTGCGATATTTGCGTTCCGCTGGGTG 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                    56;
                                                                                                                                                                                                                                                                                                    0; Mismatches
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/db_xref="taxon:9606"
/clone="IMAGE:2242420"
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                                                                                                                                                                                                                                                               16.5%;
75.7%;
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                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                   106
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VERSION
KEYWORDS
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AUTHORS
TITLE
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//note__vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library NCI_CGAP_GG4 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1257096-1258631, 1459064-1470983, and 1475592-1476743). Subtraction by Bento Soares and M. Fatima Bonaido. "

143 c 163 g 114 t 2 others
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Insert Length: 623 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AI633790 531 bp mRNA EST 14-DEC-1999 tt28el0.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2242122 3's similar to TR:016361 Q16361 CELL CYCLE NEGATIVE REGULATOR BETA FORM :contains LTR9.b3 TAR1 repetitive element ;, mRNA sequence.
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Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausbergenih.gov
Email: Robert_Strausbergenih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 531)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              234 GTAGCAGCTCTTCTGCTCAACTACGGTGCAGATTCGAACTGCGAGGACCCCACTACCTTC 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  525 GIGGCGGAGCIGCIGCICCICCACGCCGGGAGCCCAACIGCGNCGACNCCGCCACICIC 466
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 528;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 16.4%; Score 140; DB 42; Length 5 Best Local Similarity 75.2%; Pred. No. 3e-28; Matches 173; Conservative 0; Mismatches 57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="pooled_germ cell tumors"
/lab_host="DH108"
/clone_lib-"NCI_CGAP_GC6"
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High quality sequence stop: 4
Location/Qualifiers
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A1633790.1 GI:4685120
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I (Dases 1 to 480)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

I (Dupublished (1997)

On Jan 6, 2000 this sequence version replaced gi:6676951.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550

Email: Robert_Strausberg@nih.gov
Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D. CDNA Library Preparation: Life
Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The I.M.A.G.E. Consortium DNA Sequencing by: Washington University
                                                                                                                      /note="Vector: pT713D-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library NCI_CGAP_GG4 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made iform the same library (cloneIDs 1257096-1258631, 1469064-1470983, and 1475592-147643). Subtraction by Bento Soares and M. Falima Bonaldo. "

144 c 163 g 116 t lothers
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Seq primer: 40RP from Gibco
High quality sequence stop: 314.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AW631047 480 bp mRNA EST 31-WAR-2000 hb91d11.yl NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2970165 5' similar to SW:CDN2_HUWAN P42771 CYCLIN-DEPENDENT KINASE 4 INHIBITOR
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16.3%; Score 139.4; DB 42; Length 531;
Best Local Similarity 75.2%; Pred. No. 4.4e-28;
Matches 173; Conservative 0; Mismatches 57; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  414 CAAGAGCGGGGACATCAAGACATCGTGCGATATTTGCGTTCCGCTGGGTG 463
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/clone_11b="NCL_CGAP_GG6"
/tssue_type="pooled germ cell tumors"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; mRNA sequence.
AW631047
AW631047.1 GI:7377837
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                                                                                                  /lab_host="DH10B"
/note="Organ: genitourinary tract; Vector: pCMV-SPORT6;
Site_1: SalI; Site_2: NotI; Cloned unidirectionally.
Primer: Oligo dT. Library constructed by Life
                                                                                                                                                                                                                                                                                                                                              207 CAGGIGAIGAIGAIGGGCAACGIICACGIAGCAGCICTICIGCICAACIACGGIGCAGAI 266
                                                                                                                                                                                                                                                                                                                                                                    267 TCGAACTGCGAGGACCCCACTACCTTCTCCCGCCCGGTGCACGACGCAGCGCGGGAAGGC 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               327 ITCCTGGACACGCTGGTGGTGCTGCACGGGTCAGGGGCTCGGCTGGATGTGCGGATGCC 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
/db_xref="taxon:9606"
/clone="IMAGE:2970165"
/clone_lib="NCI_CGAP_GUI"
/tissue_type="2 pooled high-grade transitional cell
tumors"
                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                       Length 480;
                                                                                                                                                                                                                                                                     Score 133.4; DB 79; Length
Pred. No. 2e-26;
0; Mismatches 56; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       387 IGGGGICGCCIGCCGCTCGACIIGGCCCAAGAGCGGGGACAIC 429
                                                                                                                                                                                                                                                         15.6%; Sco. 74.9%; Pred. No. 2c. 74.9%; O; Mismatches
                                                                                                                                                                                           135 g
                                                                                                                                                                            Technologies.
144 c
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Search completed: July 21, 2000, 02:48:50 Job time: 9645 sec

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein . protein database search, using Smith-Waterman algorithm MPsrch pp

Thu Jul 20 08:41:29 2000; MasPar time 6.47 Seconds 457.636 Million cell updates/sec Run on:

Tabular output not generated.

Description: Perfect Score:

>US-09-016-869A-6 (1-125) from US09016869A.pep 892 1 MAMGNVHVAALLINYGADSN.....SFSSSTPRALELRGQSQEQS 125 Seguence:

PAM 150 Gap 11 Scoring table:

188963 seqs, 23686106 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

a-geneseq36 1:geneseqp Database:

Mean 29.993; Variance 124.567; scale 0.241 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Pred. No.	3.05e-77	3.05e-77	3.05e-77	3.90e-60	3.94e-35	3.94e-35	3.94e-35	3.94e-35	3.94e-35	3.94e-35	3.94e-35	3.94e-35	3.94e-35	3.94e-35	3.94e-35	3.94e-35	3.94e-35	3.94e-35	3.94e-35	3.94e-35	3.94e-35	3.94e-35	3.94e-35
Description	Murine INK4a-p16 C-ter	Cell-cycle regulatory	Mouse multiple tumour	Cell-cycle regulatory	A human multiple tumou	Multiple tumour suppre	Amino acid sequence 1	Human multiple tumour	Human multiple tumour	Human MTS1E1-beta prot	Multiple tumour suppre	Human multiple tumour	Inhibitor of cyclin de	Amino acid sequence of	Cell-cycle regulatory	Tumour suppressor p16.	A human multiple tumou	Human multiple tumour	Human MTS1 protein.		p27,	27/p16	Human p16p27 fusion pr
ដ	W16322	R85120	W80527	R85119	W80525	R81700	W74550	R80947	W19254	W40525	R81701	R80940	R53401	W74549	R85116	W10627	W80524	W19251	W40524	W95105	W95106	W95103	W95107
8	П	Н	Н	ч	ч	-	-	ч	Н	Н	-1	-	Н	-	Н	-	-	Н	Н	Н	н	н	н
% Query Match Length	125	125	168	127	105	105	105	105	105	105	148	148	151	156	156	156	156	156	156	237	252	m	365
% Query Match	100.0	100.0	100.0	81.1	53.0	53.0	53.0	53.0	53.0		53.0	53.0	53.0	53.0	53.0	53.0	53.0	53.0	53.0	53.0	53.0	53.0	53.0
Score	892	892	892	723	473	473	473	473	473	473	473	473	473	473	473	473	473	473	473	473	473	473	473
Result No.	н	71	m	4	'n	ø	7	ω	6	10	11	17	13	14	15	16	17	18	19	20	21	22	53

3.94e-35	3.94e-35	3.94e-35	3.94e-35	3.94e-35	3.94e-35	4.95e-35	4.95e-35	4.95e-35	4.95e-35	4.95e-35	4.95e-35	3.05e-34	6.04e-34	7.59e-34	9.52e-34	1.88e-33	3.72e-33	•	8.93e-32	8.93e-32	1.48e-27
Human p16p27 fusion pr	ry fusic	CDK inhibitory fusion	Human p16(GS)p27 fusto	Human p27-p16 fusion p	CDK inhibitory fusion	Amino acid sequence 2		Multiple tumour suppre	tiple t	A human multiple tumou	Human multiple tumour	Human multiple tumour	Mouse multiple tumour	Cell-cycle requiatory		Human multiple tumour	Truncated p27/p16 fus1	Cell-cycle regulatory			
W95096	W23536	W23535	W95095	W95094	W23534	W74553	W40526	R81702	W19255	W80526	R80948	W19252	W70823	R85117	R85118	W19253	W95104	R85113	R85115	R85114	W16324
Н	-	-	-	-	Н	-	Н	Н	н	Н	Н	Н	ч	н	Н	-	н	н	-1	н	н
365	365	380	380	391	391	138	138	138	138	138	138	156	130	138	130	156	348	82	138	157	67
53.0		53.0	'n	53.0	53.0	52.9	52.9	52.9	52.9	52.9	52.9	52.0	51.7	51.6	51.5	51.1	50.8	49.2	49.2	49.2	44.4
473	473	473	473	473	473	472	472	472	472	472	472	464	461	460	459	456	453	439	439	439	396
24	25	3 6	27	28	53	30	31	32	33	34	35	36	37	38				42		44	45

ALIGNMENTS

THE PROPERTY OF STREET OF	Wish the standard; Protein; 125 AA. Wish the standard; Protein; Ish the standard
ខ្លួន	Irequently in cancer cells, suggesting that ink4a-plb suppresses tumour formation.
3	Sequence 123 AA;

0; Gaps Score 892; DB 1; Length 125; Pred. No. 3.05e-77; 0; Mismatches 0; Indels Query Match
Best Local Similarity 100.0%;
Matches 125; Conservative

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                                                                                                                                                                                                                                                                                                                 cyclin-dependent kinase inhibitor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 RLPLDLAQERGHQDIVRYLRSAGCSLCSAGWSLCTAGNVAQTDGHSFSSSTPRALELRGQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RLPLDLAQERGHQDIVRYLRSAGCSLCSAGWSLCTAGNVAQTDGHSFSSSTPRALELRGQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MAMGNVHVAALLLINYGADSNCEDPTTFSRPVHDAAREGFLDTLVVLHGSGARLDVRDAWG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MMMGNVHVAALLLNYGADSNCEDPTTFSRPVHDAAREGFLDTLVVLHGSGARLDVRDAWG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New cell cycle regulating proteins bind to cyclin dependent kinase and related nucleic acids, antibodies etc., used in diagnosis and therapy of abnormal cell proliferation, degeneration etc.

Example 5: Page 81: 109pp; English.

The mouse cell-cycle regulatory (CCR) protein pi3.5 (R85120) was both. by expression of a CDNA clone (T02955) isolated from mouse embryonal stem cells. CCR pi3.5 specifically inhibits the activity of cyclin-dependent kinases during various stages of the cell cycle, and can be used in the treatment and diagnosis of sequence 125 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 7; Fig 19; 80pp; English.
The present sequence represents mouse multiple tumour suppressor 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    - useful for primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 892; DB 1; Length 125;
Pred. No. 3.05e-77;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mouse multiple tumour suppressor 1 (MTS1) protein.
Murine; multiple tumour suppressor 1 gene; MTS1; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                     26-OCT-1995.
14-APR-1995; U04636.
14-APR-1994; U5-227371.
25-MAY-1994; US-248812.
14-SEP-1994; US-348812.
14-SEP-1994; US-346147.
COLD-) COLD SPRING HARBOR LAB.
Beach DH, Demetrick DJ, Hannon GJ, Serrano M; WPI: 95-373798/48.
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                                                                                                                                                                                                                                                                               Cell-cycle regulatory protein pl3.5.
Cell-cycle regulatory protein pl3.5;
CCR; cancer; cell proliferation.
Mus sp.
W09528483-A1.
                                                                                                                                                        r 2
R85120 standard; Protein; 125 AA.
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W80527 standard; Protein; 168 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US5843756-A.
01-DEC-1998.
28-JUL-1995; 058735.
28-JUL-1995; US-508735.
07-JUN-1995; US-487033.
(MYRI-) MYRIAD GENETICS INC.
Jiang P, Ramb A, Stone S;
WPI; 99-044565/04.
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Best Local Similarity 100.0%;
Matches 125; Conservative
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121 SQEQS 125
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SQEQS 125
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SQEQS 125
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                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                            Cell-cycle regulatory protein homologue.
Cell-cycle regulatory protein; cyclin-dependent kinase inhibitor;
CCR; cell proliferation; agonist; antagonist.
Synthetic.
detect abnormalities i.e. polymorphisms which may predispose towards malignancies such as melanoma, leukaemia, astrocytoma, lymphoma, glioma, as well as tumours of e.g. the breast, thyroid, pancreas, uterus and kidneys.
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                                                                                                                                                                           Score 892; DB 1; Length 168;
Pred. No. 3.05e-77;
0; Mismatches 0; Indels
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'note= "unidentified amino
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//note= "unidentified amino misc_difference 18..19
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14-APR-1995; U04636.
14-APR-1994; US-227371.
25-MAY-1994; US-248812.
14-SEP-1994; US-306511.
29-NOV-1994; US-346147.
(COLD-) COLD SPRING HARBOR LAB.
Beach DH, Demetrick DJ, Hannon GJ, St
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R85119 standard; Protein; 127 AA.
                                                                                                                                                                           Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 125; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R85119;
01-MAR-1996 (first entry)
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misc_difference 49..50
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                                                                                                                                                                                                                                                                                                                                                                                                                                        164 SQEQS 168
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1 MAMGSARVAELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Detecting polymorphism associated with cancer pre:disposition - also DNA, vectors and host cells e.g. for gene or protein replacement therapy and drug screening Example 7: Page 101; 148pp; English. An individual can be diagnosed as having a predisposition to cancer by detecting an alteration in the wild type multiple tumour suppressor (MTS) gene, using gene probes which hybridise to the WTSIELbeta gene ORF 100/14 (which encodes R81700). The above assay can also be used in the diagnosis and prognosis of melanoma, lymphoma, leukaemia and pancreas, breast and thyroid cancers, etc. . Sequence 105 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 7; Column 75-76; 73pp; English.

This is the amino acid sequence of the multiple tumour suppressor (WTSIELS) protein, used in the method of the invention. The WTS gen is useful in the diagnosis and proponsis of human cancer, e.g. by standard nucleic hybridisation techniques, of patient samples. The mutated sequences are those that are present in somatic mutations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; V53830.

Nucleic acids based on multiple tumour suppressor, MTS, sequences useful as hybridisation probes, primers and recombinant production of MTS in the diagnosis and treatment of cancers related to MTS mutation(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-DEC-1998 (first entry)
Amino acid sequence 1 of the multiple tumour suppressor MTSIEIS.
Multiple tumour suppressor; MTSIEIS; human; cancer; hybridisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 473; DB 1; Length 105;
Pred. No. 3.94e-35;
14; Mismatches 8; Indels
          predisposition; melanoma; leukaemia; lymphoma; prognosis;
pancreas; breast; thyroid; exon 1.
                                                                                                                                                                                                                                                                                                                                     Skolnick MH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W74550 standard; Protein; 105 AA
                                                                                                   28-SEP-1995.

17-MAR.1995; U03537.

18-MAR.1995; U03537.

18-MAR.1994; US-215087.

18-MAR.1994; US-215086.

14-APR.1994; US-223369.

O1-JUN.1994; US-223369.

O1-JUN.1994; US-223369.

OTAMN 1994; US-223369.

OTAMN 1994; US-223369.

OTAMN 1994; US-251938.

(WYRI-) WYRIAD GENETICS INC.

(UTAH ) UNIV UTAH RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |||:||:||:|| ||:|: ||||:|:
61 RLPLDLAQERGHQDIVRYLRSAG 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      somatic mutation; gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 53.0%;
Best Local Similarity 73.5%;
Matches 61; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MYRI-) MYRIAD GENETICS INC
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07-JUN-1995; 480810.

07-JUN-1995; US-480810.

18-MAR-1994; US-215086.

18-MAR-1994; US-215087.

14-APR-1994; US-215087.

14-APR-1994; US-227369.

01-JUN-1994; US-227369.
                                                                                                                                                                                                                                                                                                                                                               WPI; 95-344626/44.
N-PSDB; T00744.
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                                                         Homo sapiens.
WO9525813-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence represents human multiple tumour suppressor IEI-beta (MTSIEI-beta) protein. Primers designed from the gene can be used to design primers to detect abnormalities i.e. polymorphisms which may predispose towards malignancies such as melanoma, leukaemia, astrocytoma, lymphoma, glioma, as well as tumours of e.g. the breast, thyroid, pancreas, uterus and kidneys.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MMMGSARVAELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWG 60
                                                                                                                                                                                                                                                                                                                                                             1 MAMGXXXVAXLLLXXGAXXNCXDPXTXXXRPVHDAAREGFLDTLVVLHXXGARLDVRDAW 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                Gaps
New cell cycle regulating proteins bind to cyclin dependent kinase and related nucleic acids, antibodies etc., used in diagnosis and therapy of abnormal cell proliferation, degeneration etc.

Disclosure; Page 4; 109pp; English.

Cell-cycle regulatory (CCR) proteins (R85116-18, R85120) have the general formula given in R85119. The CCR proteins specifically bind to cyclin-dependent kinases and function as either agonists or antagonists of cell cycle regulation.
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R81700 standard; Protein; 105 AA.
R81700;
R81700;
R81700;
R817109 (first entry)
Multiple tumour suppressor 1 exon 1 beta (MTSIElbeta) polypeptide.
Multiple tumour suppressor; MTSIElbeta; cancer; diagnosis; assay;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mouse multiple tumour suppressor gene segment - useful for primer
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                                                                                                                                                                                                                                                            81.1%; Score 723; DB 1; Length 127; 81.1%; Pred. No. 3.90e-60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8; Indels
                                                                                                                                                                                                                                                                                                              0; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-578-1999 (first entry)
A human multiple tumour suppressor 1E1-beta protein.
Human; multiple tumour suppressor 1 gene; MTS1; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 473; DB 1; I
Pred. No. 3.94e-35;
14; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            design Example 8; Fig 12A-B; 80pp; English.
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WB0525 standard; Protein; 105 AA.
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RLPLDLAOERGHODIVAYLRSAG 83
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28-JUL-1995; 058735.
28-JUL-1995; 04-508735.
07-JUN-1995; US-487033.
(MYRI-) MYRIAD GENETICS INC.
JIANG P, RAMD A, Stone S;
WPI: 99-044585/04.
N-PSDB; V70594.
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Best Local Similarity 73.5%;
Matches 61; Conservative
                                                                                                                                                                                                                                                                                   Best Local Similarity 81.1%;
Matches 103; Conservative
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US5843756-A.
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pre:disposition - also

gene

61 RLPLDLAQERGHQDIVRYLRSAG

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Wild-type multiple tumour suppressor (MTS) gene and mutant sequences

useful in diagnosis, prognosis and therapy of human cancer, e.g.
melanoma or leukaemia

Zeveral multiple tumour suppressor (MTS) polypeptides have been isolated
and sequenced. This sequence is the MTS polypeptides was leading the diagnosis or prognosis of them and mutants of these are useful for the diagnosis or prognosis of human cancer. Germ-line mutations of MTS polypeptide-encoding cDNAs and mutants of these are useful for the diagnosis or prognosis of human cancer. Germ-line mutations of MTS polypeptides and cancers of the pancreas, thyroid, ovary, uterus, testis, kidney, stomach and rectum. The wild-type gene is useful
correct therapy and MTS polypeptides or calls contg. an altered MTS gene are useful for screening for potential cancer
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gene therapy
   of the gene in cancers. The vectors can be used for gene therapy strategies to replace function of mutated protein in patients. These can also be used to construct protein mimetics, also for therapeutic strategies. In addition the expression constructs can also be used for recombinant production of MTS. Recombinant MTS can be used to screen for drugs to be used for cancer therapy, and the protein itself may also be used to restore MTS function in a cell. Sequence 105 AA;
                                                                                                                                                                                                                                          1 MMMGSARVAELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWG 60
                                                                                                                                                                                                                                                               Human multiple tumour suppressor polypeptide, MTSIE1-beta.
Multiple tumour suppressor; E1-alpha; diagnosis; cancer; leukaemia; astrocytoma; glioblastoma; Hodgkin's lymphoma; melanoma; glioma: Homo saplens.
Homo saplens.
                                                                                                                                                                                                         0; Gaps
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                                                                                                                                                                    Score 473; DB 1; Length 105
Pred. No. 3.94e-35;
14; Mismatches 8; Indels
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Pred. No. 3.94e-35;
14; Mismatches 8; Indels
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R80947 standard; Protein; 105 AA.
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Best Local Similarity 73.5%;
Matches 61; Conservative
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Local Similarity 73.5%;
Les 61; Conservative
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18-MAR-1994; US-214582.

18-MAR-1994; US-215086.

18-MAR-1994; US-215088.

18-MAR-1994; US-215087.

14-APR-1994; US-225389.

01-UUN-1994; US-251938.
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17-MAR-1995; U03316.
18-MAR-1994; US-2145
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Best Local 9
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61 RLPVDLAEELGHRDVARYLRAAA 83

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1 MOMGSARVAELLILHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWG 60

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DNA specific for Multiple Tumour Suppressor 1E1-beta gene - are useful for the diagnosis of cancers related to MTSIE1-beta mutation(s) and their treatment Claim 1: Fig 12; 72pp; English.
This sequence represents a human multiple tumour suppression protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MMMGSARVAELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWG 60
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                                                                                                         Human multiple tumour suppressor 1 Elbeta gene product.
Human; multiple; tumour; suppressor; MTS1; cancer; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human mutant multiple tumour suppressor gene sequences - for production of recombinant mutant polypeptide(s) Disclosure; Columns 73-74; 72pp; English.

The present sequence the human multiple tumour suppressor I (MTS1) Elbeta gene product, useful in cancer diagnosis. Sequence 105 AA;
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Pred. No. 3.94e-35;
14; Mismatches 8;
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W40525 standard; Protein; 105 AA.
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л 9
W19254 standard; Protein; 105
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RLPLDLAQERGHQDIVRYLRSAG
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Local Similarity 73.5%;
les 61; Conservative
                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                 01-JUN-1994; US-227369.
01-JUN-1994; US-227369.
17-MAR-1995; WO-U03537.
07-JUN-1995; US-474.
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                                                                                                                                                                                                                                                                                               18-MAR-1994; US-214582.
18-MAR-1994; US-215086.
18-MAR-1994; US-215087.
14-APR-1994; US-227369.
01-JUN-1994; US-251938.
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18.MAR-1994; US-215086.

18.MAR-1994; US-215086.

18.MAR-1994; US-215087.

14.APR-1994; US-221399.

17.MAR-1995; WO-U03316.
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wPI: 98-250421/22.
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N-PSDB; T69780.
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                                                                                10-SEP-1997
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Name A: Well (195-344401/44.)

N PSDB; 099158.

N-PSDB; 099158.

N-PSDB; 099158.

N-PSDB; 099158.

"Wild-type multiple tumour suppressor (MTS) gene and mutant sequences - useful in diagnosis, prognosis and therapy of human cancer, e.g. melanoma or leukaemia

Claim 5: Page 92-93; 156pp; English.

Claim 5: Page 92-93; 156pp; English.

Several multiple tumour suppressor (MTS) polypeptides have been isolated and sequenced. This sequence is the MTS polypeptide MTS!

MTS polypeptide-encoding CDNAs and mutants of these are useful for isolated and sequenced. This sequence is the MTS polypeptide MTS!

MTS cDNAs can be used for diagnosing predisposition to melanoma, it with cancer of the pancreas, thyroid, ovary, uterus, is lymphoma, school and rectum. The wild-type gene is useful cestis, kidney, stomed and rectum. The wild-type gene is useful cor gene therapy and MTS polypeptides may also be used for protein replacement therapy. Also the polypeptides or cells contg. an altered MTS gene are useful for screening for potential cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44 MMGSARVAELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWG 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human multiple tumour suppressor polypeptide, MTS1.
Multiple tumour suppressor; E1-alpha; dlagnosis; cancer; leukaemia; astrocytoma; glioblastoma; Hodgkin's lymphoma; melanoma; glioma; gene therapy; chronic.
WO9525429-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R53401;
07-DEC-1994 (first entry)
Inhibitor of cyclin dependent kinase 4 (p16INK4).
Cyclin: cyclin dependent kinase; CDK: oncogene; cancer; leukaemia; lymphoma; cell cycle; detection; identification; tumour virus; proliferating cell nuclear antigen; subunit; complex.
Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Detection of subunit components of cyclin complexes - used for diagnosing transformation of a cell and developing inhibitors and activators, partic for cencer treatment claim 13; Page 40; 45pp; English.

The cell cycle gene implicated most strongly in oncogenesis is the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 473; DB 1; Length 148;
Pred. No. 3.94e-35;
14; Mismatches 8; Indels
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18-007-1993; UG9945.
16-007-1992; US-963308.
17-DEC-1992; US-991997.
(COLD-) COLD SPRING HARBOR LAB.
Beach DH, Xiong Y;
WPI: 94-151320/18.
N-PSDB; Q63491.
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R53401 standard; Protein; 151 AA
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61 RLPLDLAQERGHQDIVRYLRSAG 83
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17-MAR-1995, U03316.
18-MAR-1994; US-214581.
18-MAR-1994; US-214582.
18-MAR-1994; US-215086.
18-MAR-1994; US-215088.
18-MAR-1994; US-215087.
14-APR-1994; US-227369.
01-JUN-1994; US-251938.
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Best Local Similarity 73.5%;
Matches 61; Conservative
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MTSIE1-beta. The MTS gene locus is also referred to as the familial metanoms (MLM) gene locus, located on human chromsome 9p21. Germ line mutations in MTS genes can be used in the diagnosis of predisposition to cancers, e.g. melanoma, leukaemia, astrocytoma, gliboblastoma, lymphoma, glioma, Haddkin's lymphoma, CLL, and cancers of the pancreas, breast, thyrold, ovary, uterus, testis, kidney, stomach and rectum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Detecting polymorphism associated with cancer pre:disposition - also DNA, vectors and host cells e.g. for gene or protein replacement therapy and drug screening Example 8; Pages 92-93; 148pp; English.

An individual can be diagnosed as having a predisposition to cancer by detecting an alteration in the wild type multiple tumour suppressor (MTS) gene, using gene probes which hybridise to the MTS1 gene ORF T00736 (which encodes R81701) mutant sequences T00749/50. The above assay can also be used in the diagnosis and prognosis of melanoma, lymphoma, leukaemia and pancreas, breast and thyroid
                                                                                                                                                                                                                                                                 MAMGSARVAELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWG 60
                                                                                                                                                                                                                                                                                     0; Gaps
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                                                                                                                                                                           Length 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Multiple tumour suppressor 1 (MTS1) polypeptide.
Multiple tumour suppressor; MTS1; cancer; diagnosis; assar
predisposition; melanoma; leukaemia; lymphoma; prognosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 473; DB 1; Length 148
Pred. No. 3.94e-35;
14; Mismatches 8; Indels
                                                                                                                                                                         Score 473; DB 1; Length 105
Pred. No. 3.94e-35;
14; Mismatches 8; Indels
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R80940;
03-MAY-1996 (first entry)
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17-MAR-1995; U03537.

18-MAR-1994; US-214582.

18-MAR-1994; US-215087.

18-MAR-1994; US-215086.

14-APR-1994; US-227369.

(MTR-1) MYRIAD GENETICS INC.

(UTAH ) UNIV UTAH RES FOUND.

Cannon-Albright IA, Kamb A, S
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R81701 standard; Protein; 148
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RLPLDLAQERGHQDIVRYLRSAG
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Local Similarity 73.5%;
les 61; Conservative
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Similarity 73.5%;
61; Conservative
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WO9525813-A1.
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08-May-1996
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Matches

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Gaps

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human cyclin Di. It is genetically linked to the bcl-1 oncogene, a locus activated by translocation to an immunoglobulin gene enhancer in some B-ceal lymphomas and leukaemias. D-type cyclin, cyclin dependant kinase (CDK), PCNA (proliferating cell nuclear antigen) and p21 (a 21 kDa polypeptide) exist in a quaternary complex that many combinatorial variations of the components e.g. cyclin D or D3 and CDK2, CDK4 and CDK5, assemble in vivo. Each quaternary complex may have a subtly diferent role in the cell cycle or in different cell types. Cellular transformation by DNA tumour viruses such as SV40 is associated with selective subunit rearrangement of the cyclin D complexes. In virally transformed cells, CDK4 totally dissociates from cyclin, PCNA and p21 and becomes associated with a 16 kilodalton polypeptide (p16). This sequence, designated p16IRK4, binds to and inhibits CDK4. p16INK4 was discovered to show many similarities to p16. Reagents, such as monoclonal antibodies, can be developed that recognise the interactions between the CDK's cyclins, PCNA and low molecular weight polypeptides and can therefore be used to identify squence 151 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mutation(s)

Disclosure; Column 63-64; 73pp; English.

This is the amino acid sequence of the multiple tumour suppressor I this is the amino acid sequence of the multiple tumour suppressor I this is the amino acid sequence of the multiple tumour suppressor I this is the amino acid sequence of the method of the invention. The WTS gene is useful in the diagnosis and prognosis of human cancer, e.g. by standard nucleic hybridisation techniques, of patient samples. The mutated sequences are those that are present in somatic mutations of the gene in cancers. The vectors can be used for gene therapy strategies to replace function of mutated protein in patients. These can also be used to construct protein mimetics, also for therapeutic strategies. In addition the expression constructs can also be used to recombinant the round of MTS. Recombinant MTS can be used to screen for drugs to be used for cancer therapy, and the protein itself may also be used to restore MTS function in a cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acids based on multiple tumour suppressor, MTS, sequences useful as hybridisation probes, primers and recombinant production of MTS in the diagnosis and treatment of cancers related to MTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-DEC-1998 (first entry)
Amino acid sequence of multiple tumour suppressor 1.
Multiple tumour suppressor 1; MTS-1; human; cancer; hybridisation; somatic mutation; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 473; DB 1; Length 151
Pred. No. 3.94e-35;
14; Mismatches 8; Indels
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larity 73.5%;
Conservative
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18-MAR-1994; US-215086.
18-MAR-1994; US-215087.
14-APR-1994; US-227369.
01-JUN-1994; US-251938.
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nes 61; Conser
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Cell-cycle regulatory protein p16.
Cell-cycle regulatory protein p16; cyclin-dependent kinase inhibitor;
CCR; cancer; cell proliferation.
                                                                                                                                                 52 MMMGSARVAELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWG 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52 MMMGSARVAELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWG 111
                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The human cell-cycle regulatory (CCR) protein p16 (R85116) was obtd. by expression of a CDNA clone (T02962) isolated in a 2-hybrid screening assay. CCR p16 specifically inhibits the activity of cyclin-dependent kinases during various stages of the cell cycle, and can be used in the treatment and diagnosis of proliferative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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The human cell-cycle regulatory (CCR) protein p16 (R85116) was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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Pred. No. 3.94e-35;
14; Mismatches 8; Indels
Score 473; DB 1; Length 156;
Pred. No. 3.94e-35;
                                                                            8; Indels
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                                                                            14; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                .r 15
R85116 standard; Protein; 156 AA.
R85116;
                                                                                                                                                                                                                                                                                       112 RLPVDLAEELGHRDVARYLRAAA 134
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61 RLPLDLAQERGHQDIVRYLRSAG 83
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14-58P-1994; US-306511.
29-NOV-1994; US-346147.
(COLD-) COLD SPRING HARBOR LAB.
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Similarity 73.5%;
61; Conservative
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14-APR-1995; U04636.
14-APR-1994; US-227371.
       Query Match
Best Local Similarity
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WPI; 95-373798/48.
N-PSDB; T02962.
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu Jul 20 08:43:29 2000; MasPar time 5.20 Seconds 347.144 Million cell updates/sec

Tabular output not generated.
Title: >US-09-016-869A-6
Description: (1-125) from US09016869A.pep
Perfect Score: 892

Description: (1-125) from US09016869A.pep
Perfect Score: 892
Sequence: 1 MMGNVHVAALLLNYGADSN.....SFSSSTPRALELRGQSQEQS 125

Scoring table: PAM 150 Gap 11 Cot.nroccocing. Winimum Watch Co

Searched:

145341 segs, 14437480 residues

Post-processing: Minimum Match 0% Listing first 45 summaries Database: a-issued 1:5A_COMB 2:5B_COMB 3:6_COMB 4:PCT_COMB 5:backfiles1

Statistics: Mean 28.127; Variance 120.872; scale 0.233

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result Ouery No. Score Match Length DB ID Description Pred. No. No. Score Match Length DB ID Description C. Applicatio 2.41e-75 a 892 100.0 125 4 PCT-US95-0 Sequence 6, Applicatio 2.41e-75 4 892 100.0 125 2 US-08-9306 Sequence 6, Applicatio 2.41e-75 4 892 100.0 125 2 US-08-934 Sequence 5, Applicatio 2.41e-75 6 892 100.0 125 2 US-08-581 Sequence 5, Applicatio 2.41e-75 7 892 100.0 125 2 US-08-581 Sequence 5, Applicatio 2.41e-75 8 100.0 125 2 US-08-581 Sequence 6, Applicatio 2.41e-75 1 US-08-581 Sequence 14, Application 2.41e-75 1 US-08-581 Sequence 14, Application 1.62e-34 1

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Gaps

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Score 892; DB 4; Length 125; Pred. No. 2.41e-75; 0; Mismatches 0; Indels

Query Match 100.0%; Best Local Similarity 100.0%; Matches 125; Conservative

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61 RLPLDLAQERGHQDIVRYLRSAGCSLCSAGWSLCTAGNVAQTDGHSFSSSTPRALELRGQ 120
                                                                STANDARD;
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MOLECULE TYPE: protein
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US-08-893-274-6
                121 SQEQS 125
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                                      RLPLDLAQERGHQDIVRYLRSAGCSLCSAGWSLCTAGNVAQTDGHSFSSSTPRALELRGQ 120
       1 MMGNVHVAALLLINYGADSNCEDPTTFSRPVHDAAREGFLDTLVVLHGSGARLDVRDAWG 60
               Sequence 6, Application US/08306511A
Patent No. 5962316
GENERAL INFORMATION:
APPLICANT: Beach, David H.
APPLICANT: Demetrick, Douglas J.
APPLICANT: Bennon, Gregory J.
TITLE OF INVENTION: Cell-Cycle Regulatry Proteins, and Uses
TITLE OF INVENTION: Cell-Cycle Regulatry Proteins, and Uses
ADDRESSED: LAHVES: 11
CORRESPONDENCE: 11
CORRESPONDENCE: LAHIVE 6 COCKFIELD
STREET: 60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MMMGNVHVAALLLINYGADSNCEDPTTFSRPVHDAAREGFLDTLVVLHGSGARLDVRDAWG 60
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                                                                                                                        125 AA.
                                                                                                                                                                                                                                                                                                                                                                                                    NAME: VINCERT, MATTHEW P.
REGISTRATION NUMBER: 36,709
REFERENCE, POCKET NUMBER: 36,709
RELECOMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 125 amino acids
                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/306,511A
FILING DATE: 14-SEP-1994
ATTORNEY AGENT INFORMATION:
                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII/+***
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JENCE 125 AA; 13458 MW; 73768 CN;
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                                                                                                                        STANDARD;
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Sequence 6, Application US/08893274
Patent No. 596821
GENERAL INFORMATION:
APPLICANT: Beach, David H.
APPLICANT: Serrano, Manuel
APPLICANT: Hannon, Gregory J.
TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, TITLE OF INVENTION: and Uses Related Thereto
125 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT ASCII(text)
CURRENT ASCII(text)
CURRENT ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/893,274
FILING DATE: 15-JULY-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/20,511
FILING DATE: 14-SEPTEMBER-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/22,371
FILING DATE: 14-APRIL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/22,371
FILING DATE: 14-APRIL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/154,915
FILING DATE: 11-DECEMBER-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/991,997
FILING DATE: 17-DECEMBER-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/991,997
FILING DATE: 16-OCTOBER-1992
ATTORNEY AMERICANDENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIV-071.09
                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSE: FOLEY, HOAG & ELIOT LLP
STREET: One Post Office Square
  PRT;
                                                                                                                                                      Sequence 6, Application US/08893274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION TELEPHONE: (617) 832-1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (617) 832-1000
TELEFAX: (617) 832-7000
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 125 amino acid
TYPE: amino acid
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Sequence 6, Application US/08581918A
Patent No. 6643030
GENERAL INFORMATION:
APPLICANT: Beach, David H.
APPLICANT: Beach, Manuel
APPLICANT: Berneo, Manuel
APPLICANT: Berneo, Cregory J.
TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses
TITLE OF INVENTION: Related Thereto
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: Roley, Heag & Eliot
SIREET: One Post Office Square
           125 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: GAS

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY disk

COMPUTER: END PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WordPad

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/581,918A

FILING DATE: 02-JAN-1996

FILING DATE: 30-JAN-1996

FILING DATE: 30-JAN-1996

FILING DATE: 29-NOV-1994

PRIOR APPLICATION NUMBER: US 08/46,147

FILING DATE: 29-NOV-1994

PRIOR APPLICATION DATE: BPLICATION NUMBER: US 08/346,147

FILING DATE: 25-MAY-1994

PRIOR PAPLICATION NUMBER: US 08/36,511

FILING DATE: 14-SEP-1994

PRIOR PAPLICATION NUMBER: US 08/26,511

FILING DATE: 14-SEP-1994

PRIOR PAPLICATION NUMBER: US 08/27,371

FILING DATE: 14-APR-1994

PRIOR PAPLICATION NUMBER: US 08/27,371

FILING DATE: 14-APR-1994

PRIOR PAPLICATION NUMBER: US 08/154,915

FILING DATE: 18-NOV-1993

PRIOR PAPLICATION NUMBER: US 08/154,915

FILING DATE: 11-DEC-1992

APPLICATION NUMBER: US 08/154,915

FILING DATE: 11-DEC-1992

ATTORNEY/AGENT NUMBER: US 08/154,915

FILING DATE: 11-DEC-1992
                                                                                                                                                                                                                                                                                    Sequence 6, Application US/08581918A
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                                                                                                                                                                                                     STANDARD;
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CITY: Boston
                                                                                                                                                                                                   US-08-581-918A-6
                                                                                                                    121 SQEQS 125
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Patent No. 5876965
GENERAL INFORMATION
GENERAL INFORMATION
APPLICANT: Sherr, Charles, J.
APPLICANT: Quelle, Dawn, E.
TITLE OF INVENTION: ARR-pl9, A No. 5876965el Regulator of the TITLE OF INVENTION: Marmalian Cell Cycle
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Ressler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Avenue Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OOPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/954,470
                                                                                                                                               61 RLPLDLAQERGHQDIVRYLRSAGCSLCSAGWSLCTAGNVAQTDGHSFSSSTPRALELRGQ 120
                                                                                           1 MMMGNVHVAALLLLNYGADSNCEDPTTFSRPVHDAAREGFLDTLVVLHGSGARLDVRDAWG 60
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                       Score 892; DB 2; Length 125;
Pred. No. 2.41e-75;
0; Mismatches 0; Indels
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Pred. No. 2.41e-75;
0; Mismatches 0; Indels
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CLASSIFICATION: 435
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/534,975
FILING DATE: 28-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: FOX, Samuel, L.
REGISTRATION NUMBER: 30,353
REFERENCE/POCKET NUMBER: 0656.0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
"""FFRAX: 202-371-260
                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: protein
JENCE 125 AA; 13458 MW; 73768 CN;
SEQUENCE 125 AA; 13458 MW; 73768 CN;
                                                                                                                                                                                                                                                                                                                                                      Sequence 5, Application US/08954470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS: LENGTH: 125 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.0%;
Matches 125; Conservative
                         Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 125; Conservative
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ID US-08-954-470-5
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Patent No. 5919997
GENERAL INFORMATION:
APPLICANT: Beach, David H.
APPLICANT: Serrano, Manuel
APPLICANT: Delinho, Ronald A.
TILLE OF INVENTION: Transgenic Animals Having Modified Cell-Cycle
TILLE OF INVENTION: Transgenic Animals Having Modified Cell-Cycle
TILLE OF INVENTION: Regulation
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
                                                                                                                                                                                                   61 RLPLDLAQERGHQDIVRYLRSAGCSLCSAGWSLCTAGNVAQTDGHSFSSSTPRALELRGQ 120
                                                                                                                                          1 MMMGNVHVAALLLNYGADSNCEDPTTFSRPVHDAAREGFLDTLVVLHGSGARLDVRDAWG 60
                                                                                           Gaps
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                                                         Score 892; DB 1; Length 125;
Pred. No. 2.41e-75;
0; Mismatches 0; Indels
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Pred. No. 2.41e-75;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                               167 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: SACII (text)
SOFTWARE: ASCII (text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/627,610
FILING DATE: U4-APR-1996
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: VIGEOT, MAITHEW P.
RESISTRATION NUMBER: 36,709
RESISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: 36,709
REFERENCE/DOCKET NUMBER: 36,700
TELECHONE: (617) 227-7400
TELECHONE: (617) 227-5941
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
JENCE 167 AA; 17870 MW; 131634 CN;
                                                                                                                                                                                                                                                                                                                                              PRT;
              MOLECULE TYPE: protein
JENCE 125 AA; 13458 MW; 73768 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 6, Application US/08627610
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TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                          Query Match
Best Local Similarity 100.0%;
Matches 125; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 125; Conservative
TOPOLOGY: linear
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STATE:
                             SEQUENCE
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Patent No. 5723313

GENERAL INFORMATION:
APPLICANT: Sherr, Charles, J.
APPLICANT: Quelle, Dawn, E.
TITLE OF INVENTION: ARP-p19, A No. 5723313e1 Regulator of the Mammalian Cell
TITLE OF INVENTION: Cycle
NUMBER OF SEQUENCES: 12
CORRESPONDENCE SIZE
ADDRESSE: Sterne, Ressler, Goldstein & Fox P.L.C.
STREET: 1100 New York Avenue Suite 600
                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                             1 MAMGNVHVAALLLNYGADSNCEDPTTFSRPVHDAAREGFLDTLVVLHGSGARLDVRDAWG 60
                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                      Length 125;
                                                                                                                                                                                    Score 892; DB 3; Length 125 Pred. No. 2.41e-75; 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: Floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATENTIN Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/534,975 FILING DATE: 28-SEP-1995 CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      125 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0656.0590000
REFERENCE/DOCKET NUMBER: MIV-071.06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
HENCE 125 AA; 13458 MW; 73768 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 0656
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2540
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
           TELECOMMUNICATION INFORMATION:
TELEPRONE: (617) 832-1299
TELEPRY: (617) 832-7000
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH : 125 antho acids
TYPE: antho acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: ...
ATTORNEY, AGENT INFORMATION:
NAME: FOX, Samuel, L.
REGISTRATION NUMBER: 30,353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       125 amino acids
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Best Local Similarity 100.0%;
Matches 125; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: D.C.
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US-08-534-975-5
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Best Local Similarity 100.0%; Pred. No. 2.41e-75;
Matches 125; Conservative 0; Mismatches 0; Indels
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US-08-581-918A-14
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ZIP: 02109
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                  Sequence 46, Application US/08508735
Patent No. 5843756
GENERAL INFORMATION:
APPLICANT: Stone, Steven
APPLICANT: Stone, Steven
APPLICANT: Stone, Ping
APPLICANT: Mamb, Alexander
TITLE OF INVENTION: MTS GENE AND THERAPEUTIC USE THEREOF
NUMBER OF SEQUENCES: 47
CORRESPONDENCES: 47
CORRESPONDENCES: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
CITY: Weshington
STATE: DC
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 168;
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MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/508,735
                                                                                                                                                                                                                                                                                                                                  168 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PELLING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION NUMBER: US to be assigned FILING DATE: 07-JUN-1995
PRIOR APPLICATION NUMBER: US to be assigned FILING DATE: 17-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Inhen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 28,957
REFERENCE/D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
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168 AA; 17901 MW; 133219 CN;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 46, Application US/08508735
                                                                                                                                                                                                                                                                                                                                  STANDARD;
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MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                           JT 8
US-08-508-735-46
                                                                                                                                                                                                SQEQS 167
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APPLICANT: Beach, David H.
APPLICANT: Bemetrick, Douglas J.
APPLICANT: Serrano, Manuel
APPLICANT: Hannon, Gregory J.
TITLE OF INVENTION: Related Thereto
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley, Hoag & Ellot
STREET: One Post Office Square
CITY: Boston
STATE: MA
                                                   44 MMMGNVHVAALLLNYGADSNCEDPTTFSRPVHDAAREGFLDTLVVLHGSGARLDVRDAWG 103
0; Gaps
                                                                              127 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPad
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/581,918A
FILING DATE: 02-JAN-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/497,214
FILING DATE: 30-JUN-1995
FILING DATE: 30-JUN-1995
FILING DATE: 12-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/346,147
FILING DATE: 14-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/248,812
FILING DATE: 14-SEP-1994
PRIOR APPLICATION NUMBER: US 08/227,371
FILING DATE: 14-APR-1994
PRIOR APPLICATION NUMBER: US 08/227,371
FILING DATE: 11-APR-1994
PRIOR APPLICATION NUMBER: US 08/154,915
FILING DATE: 11-APR-1994
PRIOR APPLICATION NUMBER: US 08/154,915
FILING DATE: 18-NOV-1993
PRIOR APPLICATION NUMBER: US 08/154,915
FILING DATE: 11-DEC-1992
APPLICATION NUMBER: US 08/154,915
FILING DATE: 11-DEC-1992
APPLICATION NUMBER: US 08/154,915
FILING DATE: 11-DEC-1992
ATORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 14, Application US/08581918A
Patent No. 6043030
GENERAL INFORMATION:
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USA
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US-08-581-918A-38
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                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                    Query Match
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Matches
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                                                                                                                                                                                                              61 GRLPXDLAXEXGHXDXXXYLRXAXGCSLCSAGWSLCTAGNVAQTDGHSFSSSTPRALELR 120
                                                                                                                                                                                     1 MAMGXXXVAXLLLXXGAXXNCXDPXTXXXRPVHDAAREGFLDTLVVLHXXGARLDVRDAW 60
                                                                                                                                                           2; Gaps
                                                                                                                                                                                                                                                                                                                                                               Sequence 39, Application US/08581918A
Patent No. 6043030
GENERAL INFORMATION:
APPLICANT: Beach, David H.
APPLICANT: Serrano, Manuel
APPLICANT: Serrano, Manuel
APPLICANT: Hannon, Gregory J.
TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses
TITLE OF INVENTION: Related Thereto
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
                                                                                                                                         Score 723; DB 3; Length 127;
Pred. No. 9.07e-59;
0; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                     85 AA.
NAME: Vincent, Matthew P.
REGISTRATION UNBER: 36,709
REFERENCE/DOCKET NUMBER: MIV-071.06
TELECOMUNICATION INFORMATION:
TELEPAX: (617) 832-1299
TELEFAX: (617) 832-1290
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 127 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPad
CURRENT APPLICATION DATA:
APPLICATION NATA:
FILING DATE: 02-JAN-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/497,214
FILING DATE: 30-JUN-1995
FILING DATE: 30-JUN-1995
APPLICATION DATA:
APPLICATION NUMBER: US 08/346,147
                                                                                              TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
JENCE 127 AA; 13611 MW; 89090 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Foley, Hoag & Ellot
STREET: One Post Offlice Square
CITY: Boston
STATE: MA
                                                                                                                                                                                                                                                                                                                                                       Sequence 39, Application US/08581918A
                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                          Query Match
Best Local Similarity 81.1%;
Matches 103; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
                                                                                                                                                                                                                                                                                           JT 10
US-08-581-918A-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: UZIP: 02109
                                                                                                                                                                                                                                                            119 GQSQEQS 125
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                                                                                                                        SEQUENCE
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Sequence 38, Application US/O8581918A
Patent No. 6043030.
GENERAL INFORMATION:
APPLICANT: Beach, David H.
APPLICANT: Serrano, Manuel, APPLICANT: Serrano, Manuel, APPLICANT: Bannon, Gregory J.
TILLE OF INVENTION: Related Thereto
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley, Hoag & Eliot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MAMGNVHVAAALLLINYGADSNCEDPTTFSRPVHDAAREGFLDTLVVLHGSGARLDVRDAWG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MMMGNVHVAALLLNYGADSNCEDPTTFSRPVHDAAREGFLDTLVVLHGSGARLDVRDAWG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 621; DB 3; Length 85;
Pred. No. 7.98e-49;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88 AA.
FILING DATE: 29-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/306,511
FILING DATE: 14-SEP-194
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/248,812
FILING DATE: 25-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,371
FILING DATE: 14-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/154,915
FILING DATE: 18-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/991,997
FILING DATE: 17-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: VINCENT, MATTHEW P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIV-071.06
TELECOMMUNICATION INFORMATION:
TELEFAX: (617) 832-1299
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH SA MAIND ACIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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STREET: One Post Office Square
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 38, Application US/08581918A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide
JENCE 85 AA; 9307 MW; 32299 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           y Match
Local Similarity 100.0%;
hes 85; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
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4 MMMGSARVAELLILLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWG 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
  TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses TITLE OF INVENTION: Related Thereto NUMBER OF SEQUENCES: 39
CORRESPONDENCE. ADDRESS:
ADDRESSEE: Foley, Hoaq & Ellot STREET: One Post Office Square CITY: Booston STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 53.0%; Score 473; DB 3; Length 89; Best Local Similarity 73.5%; Pred. No. 1.62e-34; Matches 61; Conservative 14; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   105 AA
                                                                                                                                                                         COUNTRY:

COUNTRY:

COMPUTER READABLE FORM:

MEDIUM TYEE: Floppy disk
COMPUTER: IDM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: WORDER
CLEASIFICATION DATA:
APPLICATION NUMBER: US/08/581,918A
FILING DATE: 02-JAN-1996
CLEASIFICATION NUMBER: US 08/497,214
FILING DATE: 30-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/346,147
FILING DATE: 39-NOV-1994
PRIOR APPLICATION NUMBER: US 08/346,147
FILING DATE: 14-SEP-1994
PRIOR APPLICATION NUMBER: US 08/248,812
FILING DATE: 25-MAY-1994
PRIOR APPLICATION NUMBER: US 08/227,371
FILING DATE: 14-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,371
FILING DATE: 11-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/154,915
FILING DATE: 11-APR-1994
PRIOR APPLICATION NUMBER: US 08/154,915
FILING DATE: 17-DEC-1992
APPLICATION NUMBER: 36,709
RESISTRATION NUMBER: 36,709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: peptide
JENCE 89 AA; 9595 MW; 32427 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64 RLPVDLAEELGHRDVARYLRAAA 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |||:||:| ||:| ||:|: ||||:|: 61 RLPLDLAQERGHQDIVRYLRSAG 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                     USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-120-130-14
                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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ID US-
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AC XXX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 473; DB 3; Length 88;
Pred. No. 1.62e-34;
14; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      89 AA.
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordpad
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/581,918A
FILING DATE: US-JAN-1996
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/306,511
FILING DATE: 14-5EP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,371
FILING DATE: 14-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,371
FILING DATE: 14-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/154,915
FILING DATE: 11-DEC-1992
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: US 07/991,997
FILING DATE: 17-DEC-1992
ATTORNEY/AGENT INFORMATION:
RECISTRATION NUMBER: MIV-071.06
REFERENCE/DOCKET NUMBER: MIV-071.06
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION FOR SEQ ID NO: 38:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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Patent No. 6043030
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Beach, David H.
PSPLICANT: Demetrick, Douglas J.
APPLICANT: Serrano, Manuel
APPLICANT: Hannon, Gregory J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 37, Application US/08581918A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE 88 AA; 9526 MW; 31729 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64 RLPVDLAEERGHRDVAGYLRTAA 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |||:|||:|||:||||:|:
61 RLPLDLAQERGHQDIVRYLRSAG 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 88 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 53.0%;
Best Local Similarity 73.5%;
Matches 61; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JT 12
US-08-581-918A-37
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Sequence 14, Application US/08486047
Patent No. 5994010
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Kamb, Alexander
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
CITY: Washington
STREE: DC
                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:

MEDLUM TYPE: Floppy disk
MEDLUM TYPE: Floppy disk
MEDLUM TYPE: Floppy disk
COMPUTER: INW PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: Patentin Release #1.0, Version #1.30
CURSENT APPLICATION DATA:
APPLICATION NUMBER: U5/08/486,047
FILING DATE: 07-JUN-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: CCT/US95/03316
FILING DATE: 11-AMR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,938
FILING DATE: 01-UN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-ARR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,086
FILING DATE: 14-ARR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,086
FILING DATE: 14-ARR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-MR-1994
ATONNEY ABPLICATION DATA:
APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-MR-1994
ATONNEY ABPLICATION DATA:
APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-MR-1994
ATONNEY ABOUT INFORMATION:
TELEPHONE: 202-962-4810
TELEPHONE: 202-962-4810
                                                                                                                     Sequence 14, Application US/08486047
                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                 USA
JT 14
US-08-486-047-14
                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                               Sequence 14, Application US/09120130
Patent No. 6037462
GENERAL INFORMATION:
APPLICANT: Kamb, Alexander
TITLE OF INVENTION: WTS1 GENE
NUMBER OF SEQUENCES: 36
CORRESPONDENCE JADDRESS:
ADDRESSE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 53.0%; Score 473; DB 3; Length 105; Best Local Similarity 73.5%; Pred. No. 1.62e-34; Matches 61; Conservative 14; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                        ZIP: 10005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
APPLICATION NUMBER: US/09/120,130
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24884-109348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRICIA DATE:
PRICIA APPLICATION DATA:
APPLICATION NUMBER: US 08/251,938
FILING DATE: 01-070-1994
PRICIA APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-MAR-1994
PRICIA APPLICATION DATA:
APPLICATION NUMBER: US 08/215,086
FILING DATE: 18-MAR-1994
PRICIA APPLICATION DATA:
APPLICATION NUMBER: US 08/227,369
FILING DATE: 18-MAR-1994
PRICIA APPLICATION DATA:
APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-MAR-1994
ATTORNET ABELICATION NUMBER: 28,957
REGISTRATION NUMBER: 28,957
REGISTRATION NUMBER: 28,957
REGISTRATION NUMBER: 28,957
REGISTRATION NUMBER: 24,984-10934
TELECOMMUNICATION NUMBER: 24,984-10934
TELECOMMUNICATION NUMBER: 24,984-10934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
FENCE 105 AA; 11215 MW; 43370 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/480,810
                                                  Sequence 14, Application US/09120130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 105 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                         CITY: Washington
STATE: DC
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                          Score 473; DB 2; Length 105; Pred. No. 1.62e-34; 14; Mismatches 8; Indels
                                                                                                        MOLECULE TYPE: protein
ENCE 105 AA; 11215 MW; 43370 CN;
INFORMATION FOR SEQ ID NO: 14: SEQUENCE CHARACTERISTICS: LENGTH: 105 amino acids TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                61 RLPVDLAEELGHRDVARYLRAAA 83
                                                                                                                                                         Query Match 53.0%;
Best Local Similarity 73.5%;
Matches 61; Conservative
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61 RLPVDLAEELGHRDVARYLRAAA 83 |||:|||:|| ||:|: ||||:|: | RLPLDLAQERGHQDIVRYLRSAG 83

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61 RLPLDLAQERGHQDIVRYLRSAG 83

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Sequence 14, Application US/08474177
Patent No. 56249
CREERAL HOROMATION:
APPLICANT: Skolnick; Mark H.
APPLICANT: Skolnick; Mark H.
APPLICANT: Cannon-Ablight, Lisa A.
ADDRESSED: Venable, Bacter, Howard & Civiletti, LLP
CITY: Washington
STREET: 1201 New York Avenue, Suite 1000
CITY: Washington
STREET: 12005
CONNETR: Plan PC compatible
CONNETR: Patentin Release #1.0, Version #1.30
CONPUTER: READABLE FORM:
MEDIUM TYPE: Ploppy disk
CONPUTER: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,177
FILING DATE: 17-MAR.1994
FRIUM SAPLICATION NUMBER: US 08/251,938
FILING DATE: 10-TON-1994
PRIOR APPLICATION NUMBER: US 08/215,086
FILING DATE: 10-TON-1994
PRIOR APPLICATION NUMBER: US 08/215,086
FILING DATE: 18-MAR.1994
APPLICATION NUMBER: US 08/215,086
FILING DATE: 18-MAR.1994
APPLICATION NUMBER: US 08/215,086
FILING DATE: 18-MAR.1994
APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-MAR.1994
APPLICATION NUMBER: US 08/217,369
FILING DATE: 18-MAR.1994
APPLICATION NUMBER: 28-957
RESEISRATION NUMBER: 28-957
RESEISRATION NUMBER: 28-957
RESEISRATION NUMBER: 28-958
RESEISRATION OF SEQUENCE CHARACTERISTICS:
LEGGENGUAL OF SEQUENCE CHARACTERISTICS:
LEGGENGUAL OF SEQUENCE CHARACTERISTICS:

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Pred. No. 1.62e-34;
14; Mismatches 8; Indels
                   105 AA.
                   PRT;
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JENCE 105 AA; 11215 MW; 43370 CN;
                                                                                                                       Sequence 14, Application US/08474177
                   STANDARD;
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Best Local Similarity 73.5%;
Matches 61; Conservative
 US-08-474-177-14
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Gaps

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein · protein database search, using Smith-Waterman algorithm

Thu Jul 20 08:41:56 2000; MasPar time 10.59 Seconds 556.609 Million cell updates/sec Run on:

Tabular output not generated.

>US-09-016-869A-6 (1-125) from US09016869A.pep 892 1 MAMGNVHVAALLLNYGADSN.....SFSSSTPRALELRGQSQEQS 125 Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

142080 seqs, 47172406 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

pir63 1:pir1 2:pir2 3:pir3 4:pir4 Database:

Mean 41.141; Variance 75.478; scale 0.545 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Pred. No.	2.02e-169	4.04e-76	6.66e-76	1.62e-73	7.47e-26	7.19e-25	6.47e-23	6.47e-23	4.56e-19	4.05e-18	2.58e-11	5.86e-11	4.46e-10	6.67e-10	6.67e-10	9.97e-10	9.97e-10	1.49e-09	1.62e-08	3.56e-08	3.56e-08	7.79e-08	7.79e-08
Description	p16INK4a - mouse	cyclin dependent kina	CDK4 inhibitor p14(IN	p15INK4b - mouse	cyclin-dependent kina	gene pl5INK4B protein	cyclin-dependent kina	CDK4/CDK6 inhibitor p	CDK4/CDK6 inhibitor p	CDK6 inhibitor p18 -	notch protein homolog	notch protein homolog	Notch-1 protein - mou	notch2 protein homolo	cell-fate determining	notch 3 protein - mou	notch3 protein - huma	transmembrane protein	ankyrin 2, neuronal l	death-associated prot	Xotch protein - Afric	ankyrin, erythrocyte	ankyrin 1, erythrocyt
A	158352	JE0141	B55479	I78845	A57378	152720	B57378	A57379	B57379	A55479	S18188	A40043	A46019	A56695	A49128	S45306	S78549	S42612	S37431	137275	A35844	S37771	B35049
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Length DB	167	156	138	130	164	41	166	166	168	168	2531	2555	2531	638	2471	2318	2321	2437	3924	1423	2524	1848	1856
% Query Match	100.0	53.0	52.9	51.7	26.1	25.6	24.4	24.4	22.2	21.6	17.5	17.3	16.7	16.6	16.6	16.5	16.5	16.4	15.7	15.5	15.5	15.2	15.2
Score	892	473	472	461	233	228	218	218	198	193	156	154	149	148	148	147	147	146	140	138	138	136	136
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#journal Nature (1993) 366:704-707
#title A new regulatory motif in cell-cycle control causing specific inhibition of cyclin D/CDK4.
#cross-references WUD:94081956
#accession S39359
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Harsbhan, K.; Tavtiqian, S.V.; Stockert, E.; Day III, R.S.;
Johnson, B.E.; Skolnick, M.H.
Science (1994) 264:436-440
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Chinese J. Biotechnol. (1997) 13:105-107
Molecular cloning and sequencing of P16 ink4 cDNA from hela
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                                                    Huang, C.G.; Deng, W.; Fu, J.L.
Chinese J. Biotechnol. (1997) 13:105-107
Molecular cloning and sequencing of P16ink4 cDNA from hela
cell.
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this sequence has been corrected in reference I59268
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#length 156 #molecular-weight 16532 #checksum 6490
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                                   JE0141; I59268; S39359; I59585; JC5679
                                                                                                                                                                                                                                                                                                                                                                     ##status
##molecule_type_DNA
##residues 1-152 ##label RES
##cross_references GB:S74222; NID:g710467
##cross_references GB:S74222; nide of this report is a correction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  *residues 51-152 ##label RE2
*cross-references GB:S69804; NID:9546272
Documents JC5679
                                                                                                                                                                  ##experimental_source Hella cell
NCE 159268
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                 26-Aug-1999
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##residues 1-156
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52 MAMGSARVAELLLIHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWG 111

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Ramb, A.; Gruis, N.A.; Weaver-Feldhaus, J.; Liu, Q.;
Harsbman, K.; Tavtigian, S.V.; Stockert, E.; Day III, R.S.;
Johnson, B.E.; Scolnick, M.H.
Science (1994) 264:436-440
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##residues 1-19,'Tp',22,24-31,'HSW',35-138 ##label HAN
##cross-references GB:L36844; NID:9556197; PIDN:AAA50282.1; PID:9556198
##experimental_source HaCaT cells
                                                                                                                                                                       B55479 #type complete
CDK4 inhibitor pl4(INK4B/MTS2) - human
CDK6-associated protein pl5(INK4B): cyclin-dependent kinase
inhibitor 2B; multiple tumor suppressor 2
#formal_name Honon sapiens #common_name man
23.Mar-1995 #sequence_revision 23-Mar-1995 #text_change
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##residues
1-138 ##label GUA
##cross-references GB:U17075; NID:g639715; PID:g639716
##experimental_source HeLa cells
##experimental_source HeLa cells
##authors Hannon, G.J.; Beach, D.
#journal Nature (1994) 371:257-261
#title p15(INK4B) is a potential effector of TGF-beta-induced cell
cycle arrest.
#cross-references MUID:94359613
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Papadopoulos, N.; Markowitz, S.; Willson, J.K.; Kinzler,
K.W.; Vogelstein, B.
#journal Cancer Res. (1994) 54:6353-6358
#title Deletion of p16 and p15 genes in brain tumors.
#cross_references_MUID:95079408
                                                                                                                                                                                                                                                                                                                                                                                                             #authors Guan, K.L.; Jenkins, C.W.; Li, Y.; Nichols, M.A.; Wu, X.; O'Reefe, C.L.; Matera, A.G.; Xiong, Y.
#journal Genes Dev. (1994) 8:2939-2952
#title Growth suppression by pl8, a p16(INK4/MTS1)- and p14
(INK4B/MTS2) related CDK6 inhibitor, correlates with wild-type prof. inhibitor, correlates with wild-type MTS2).
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#length 138 #molecular-weight 14722 #checksum 1236
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#map_position 9p21-9p21
KEYWORDS cell cycle control; protein kinase inhibitor; tumor
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##molecule_type DNA
#residuale_type 1-52 ##label RES
##residuale_type BRS ##cross-references GB:875756; NID:9861470
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A55479
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##residues 53-138 ##label KAM
##cross-references GB:S69805; NID:9546273
112 RLPVDLAEELGHRDVARYLRAAA 134
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61 RLPLDLAQERGHQDIVRYLRSAG 83
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#length 164 #molecular-weight 17362 #checksum 5271
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Identification of human and mouse pl9, a novel CDK4 and CDK6
Inhibitor with homology to pl6(ink4).
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                                                                               MMMGSARVAELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWG 113
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                                                                                              Hannon, G.J.; Rehberger, P.A.
Walker, C.; Beach, D.; Sherr,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ab/378 #type complete cyclin-dependent kinase inhibitor pl9 - human #formal_name Homo sapiens #common_name man 08-Feb-1996 #sequence_revision 08-Feb-1996 #text_change A57378
                                                   Gaps
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02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change
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#length 130 #molecular-weight 13788 #checksum
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                  Length 138
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              Score 472; DB 2; Length 138
Pred. No. 6.66e-76;
13; Mismatches 8; Indels
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Pred. No. 1.62e-73;
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Trono, D.; Richter, K.H.; Walk
C.J.; Serrano, M.
Oncogene (1995) 11:635-645
Cloning and characterization of
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RLPLDLAQERGHQDIVRYLRSA 82
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p15INK4b - mouse
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             Query Match
Best Local Similarity 74.4%;
Matches 61; Conservative
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Best Local Similarity 73.2%;
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#authors Chan, F.K.M.; Zhang, J.; Cheng, L.; Shapiro, D.N.; Winoto, A. #journal Mol. Cell. Biol. (1995) 15:2682-2688
#title Identification of human and mouse p19, a novel CDK4 and CDK6 inhibitor with homology to p16(ink4).
#cross-references WulD:95257949
#accession B57378
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Cancer Res. (1995) 55:1607-1612
Association of rat p15:INK4B/p16:INK4 deletions with monosomy 5
in kidney epithelial cell lines but not primary renal
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CLASSIFICATION #superfamily unassigned ankyrin repeat proteins; ankyrin
repeat homology; EGF homology and repeat proteins; SURMARX #length 166 #molecular-weight 17920 #checksum 3767
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                                                                                                      48 MMFGSTAIALELLKQGASPNVQDTSG-TSPVHDAARTGFLDTLKVLVEHGADVNVPDGTG 106
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cyclin-dependent kinase inhibitor p19 - mouse
#formal_name Mus musculus #common_name house mouse
08-Feb-1996  #sequence_revision 08-Feb-1996 #text_change
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#formal_name Rattus sp. #common_name rat
26-unl-1996 #sequence_revision 26-Jul-1996 #text_change
28-Feb-1997
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##molecule_type DNA
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Pred. No. 6.47e-23;
13; Mismatches 27; Indels
Score 233; DB 2; Length 164;
Pred. No. 7.47e-25;
15; Mismatches 29; Indels
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Pred. No. 7.19e-25;
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#length 41 #checksum 3296
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##status
##molecule_type mRNA
##molecule_type TRNA
##molecule_type TRNA
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Best Local Similarity 48.1%;
Matches 38; Conservative
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Best Local Similarity 70.7%;
Matches 29; Conservative
Query Match 26.1%;
Best Local Similarity 46.5%;
Matches 40; Conservative
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Novel INK4 proteins, p19 and p18, are specific inhibitors of the cyclin D-dependent kinases CDK4 and CDK6.
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hittle Novel INK4 proteins, p19 and p18, are specific inhibitors of
the cyclin D-dependent kinases CDK4 and CDK6.
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49 MMFGSPAVALELLKQGASPNVQDASG-TSPVHDAARTGFLDTLKVLVEHGADVNALDSTG 107
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                  B57379 #type complete
CDK4/CDK6 inhibitor p18 - mouse
#formal_name Mus musculus #common_name house mouse
08-Feb-1996 #sequence_revision 08-Feb-1996 #text_change
20-Sep-1999
                                                                                                                                                           A57379 #type complete CDE4/CDE6 inhibitor pl9 - mouse #formal_name Mus musculus #common_name house mouse 8*formal_name Mus musculus #common_name house mouse 8*formal_name Mus musculus #common_name house mouse 8*formal_name Mus musculus #common_name house mouse 20_2ep-1999
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#length 166 #molecular-weight 17894 #checksum 3512
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Pred. No. 4.56e-19;
18; Mismatches 29; Indels
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Pred. No. 6.47e-23;
13; Mismatches 27; Indels
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##molecule_type mRNA
##residues
                                                                108 SLPIHLAIREGHSSVVSFL 126
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Best Local Similarity 42.0%;
Matches 37; Conservative
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Local Similarity 48.1%;
nes 38; Conservative
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CDK6 inhibitor pl8 - human

CDK6 inhibitor pl8 - human

cyclin-dependent Kinase inhibitor 2C; D-type cyclin-dependent

kinase CDK6 inhibitor plane man

23-mar-1995 #sequence_revision 23-mar-1995 #text_change
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##cross-references GB:U17074; NID:9639713; PIDN:AAC50074.1; PID:9639714
45 MKLGNPEIARRLLLR-GANPNLKDGTGFA-VIHDAARAGFLDTVQALLEFQADVNIEDNE 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Guan, K.L.; Jenkins, C.W.; Li, Y.; Nichols, M.A.; Wu, X.; O'Keefe, C.L.; Matera, A.G.; Xiong, Y. Genes Dov. (1994) 8:2393-2952 Genes Dov. (1994) 8:2393-2952 Growth suppression by pl8, a p16(INK4/MIS1)- and p14 (INK4D/MIS2)-related CDK6 inhibitor, correlates with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 45 MKLGNPEIARRLLLR-GANPDLKDRTGFA-VIHDAARAGFLDTLGTLLEFQADVNIEDNE 102
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##molecule_type mrnn
##residues 1-2531 ##label WEI
##cross-references EMBL:X57405; NID:957634; PID:957635
##cross-references EMBL:X57405; NID:957634; PID:977635
CLASSIFICATION #superfamily unassigned ankyrin repeat proteins; ankyrin
repeat homology; EGF homology
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#map_position 1p32-1p32
CLASSIFICATION #superfamily unassigned ankyrin repeat proteins; ankyrin
                                  Weinmaster, G.; Roberts, V.J.; Lemke, G.
Development (1991) 113:199-205
A homolog of Drosophila Notch expressed during mammalian
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notch protein homolog - rat
#formal_name Rattus norvegicus #common_name Norway rat
19.Feb-1994 #sequence_revision 10-Nov-1995 #text_change
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#length 168 #molecular-weight 18127 #checksum 9379
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Pred. No. 4.05e-18;
13; Mismatches 28; Indels
                                                                                                                103 GNLPLHLAAKEGHLPVVEFLMKHTACNV 130
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#cross-references MUID:95095079
#accession A55479
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60 GRLPLDLAQERGHQDIVRYL-RSAGCSL
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#cross-references MVID:92111383
#accession S18188
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Best Local Similarity 45.0%;
Matches 36; Conservative
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A40043
Ellisen, L.W.; Bird, J.; West, D.C.; Soreng, A.L.; Reynolds, T.C.; Smith, S.D.; Sklar, J.
Cell (1991) 66:649-661
TAN-1, the human homolog of the Drosophila Notch gene, is broken by chromosomal translocations in T lymphoblastic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A40043 #type complete notch protein homolog TAN-1 precursor - human #formal_name Homo sapiens #common_name man 21-Apr-1992 #sequence_revision 21-Apr-1992 #text_change 13-Aug-1999
                                                                               #domain ankyrin repeat homology #label ANI\
#domain ankyrin repeat homology #label AN2\
#domain ankyrin repeat homology #label AN3\
#domain ankyrin repeat homology #label AN4\
#domain ankyrin repeat homology #label AN4\
#domain ankyrin repeat homology #label AN5\
#length 2531 #molecular-weight 270907 #checksum 2705
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#domain EGF homology #label EGX2,
#domain EGF homology #label EGF3,
#domain EGF homology #label EGF3,
#domain EGF homology #label EGX3,
#domain ankyrin repeat homology #label ANI,
#demain ankyrin repeat homology #label ANI,
#length 2555 #molecular-weight 272337 #checksum 463
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                                                                                                                                                                                                                                             17.5%; Score 156; DB 2; Length 2531; larity 42.9%; Pred. No. 2.58e-11; Conservative 12; Mismatches 31; Indels
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EGF1/
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#domain EGF homology
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#authors del Amo, F.F.; Gendron-Maguire, M.; Swiatek, P.J.; Jenkins,
N.A.; Copeland, N.G.; Gridley, T.
#journal Genomics (1993) 15:259-264
#title Cloning analysis, and chromosomal localization of Notch-1, a
mouse homolog of Drosophila Notch.
#cross-references MUID:93194170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gridley, T. submission submitted to the EMBL Data Library, April 1992 #description Expression pattern of Motch, a mouse homolog of Drosophila Notch, suggests an important role in early postimplantation mouse development.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ##molecule_type nucleic acid
##residues 1-2531 ##label DEL
##cross-references GB:211886; GB:S47228; NID:9288502; PIDN:CAA77941.1;
##cross-reference PID:92888503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence extracted from NCBI backbone (NCBIP:127318)
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#superfamily unassigned ankyrin repeat proteins; ankyrin
repeat homology; EGF homology
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                                                                                                                                                                                     #formal_name Mus musculus #common_name house mouse 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 20-Sep-1999 446019; $25144 A46019
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Gendron-Maguire, M.; Greenspan, R.J.; McMahon, A.P.;
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ankyrin repeat homology #label AN3\
ankyrin repeat homology #label AN4\
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#domain ankyrin repeat
#domain ankyrin repeat
#length 2531 #molecular-wel
                                           A46019 #type complete
Notch-1 protein - mouse
motch protein
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ##status preliminary; not compared with conceptual translation ##molecule_type mRNA | ##molecule_type mRNA | 1-638 ##label STI | ##residues ##cross-references GB:M99437; NID:g189263; PIDN:AAA36377.1; PID:g189264
                                                                        2027 VNNVDAAVVLLKNGANKDIENNKEETSLFLSIRRESYETAKVLLDHFANR-DITDHMDRL 2085
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                                                                                                                                                                                                                                                                                                              #formal_name Homo sapiens #common_name man
21-Jul-1995 #sequence_revision 28-Jul-1995 #text_change
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Score 149; DB 2; Length 2531;
Pred. No. 4.46e-10;
15; Mismatches 32; Indels
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submitted to the EMBL Data Library, March 1996
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#domain ankyrin repeat homology #label AN5\
#length 2471 #molecular-weight 265367 #checksum 5929
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##experimental_source Schwann cell
##note sequence extracted from NCBI backbone (NCBIP:127811)
FFICATION #superfamily unassigned ankyrin repeat proteins; ankyrin
repeat homology; EGF homology
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A49128
Weinmaster, G.; Roberts, V.J.; Lemke,
                                                           #journal Development (1992) 116:931-941
httitle Notch2: a second mammalian Notch gene.
#cross-reference MID:93202015
#accession A49128
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protein - protein database search, using Smith-Waterman algorithm MPsrch_pp

Thu Jul 20 08:42:25 2000; MasPar time 6.55 Seconds 581.041 Million cell updates/sec Tabular output not generated. Run on:

>US-09-016-869A-6 (1-125) from US09016869A.pep 892 1 MAMGNVHVAALLLNYGADSN.....SFSSSTPRALELRGQSQEQS 125 Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

83857 seqs, 30454973 residues Searched:

summaries Post-processing: Minimum Match 0% Listing first 45

Database:

swiss-prot38 1:swissprot

Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Mean 42.143; Variance 68.215; scale 0.618

SUMMARIES

	Pred. No.	1.00e-191	3.49e-86	6.14e-86	3.05e-83	2.90e-82	1.19e-76	1.91e-29	3.88e-26	8.29e-22	9.66e-21	4.22e-13	1.06e-12	1.03e-11	2.53e-11	3.97e-11	5.74e-10	5.74e-10	1.39e-09	1.39e-09	3.33e-09	3.33e-09	3.01e-06	4.54e-06
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                                                                                                                                            43 MMMGNVHVAALLLINYGADSNCEDPTTFSRPVHDAAREGFLDTLVVLHGSGARLDVRDAWG 102
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P42771; 015191;
01-N0V-1995 (Rel. 32, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
CYCLIN-DEPENDENT KINASE 4 INHIBITOR A (CDK41) (P16-INK4)
CDKNIR-LE TUMOR SUPPRESSOR 1) (MILIPLE TUMOR SUPPRESSOR 1) (MISI).
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                                                                                                    Gaps
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"A new regulatory motif in cell-cycle control causing specific
inhibition of cyclin D/CDK4.";
Nature 366:704-707(1993).
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Kamb A., Gruis N.A., Weaver-Feldhaus J., Liu Q., Harshman K.,
Tavtigian S.V., Stockert E., Day R.S. III, Johnson B.E.,
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Eukaryota; Metazoa, Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Hara E., Smith R., Parry D., Tahara H., Stone S., Peters G.;
"Regulation of pi6cDKN2 expression and its implications for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF COMPLEX WITH CDK6.
                                                          Score 892; DB 1; Length 167;
Pred. No. 1.00e-191;
0; Mismatches 0; Indels
  MISSING (IN SHORT ISOFORM)
88C4588A105ECB8F CRC64;
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Smith-Soerensen B., Hovig E.;
"CDKN2A (p16INK4A) somatic and germline mutations.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mol. Cell. Biol. 16:859-867(1996)
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Dracopoli N.C., Fountain J.W.;
"CDKNZ mutations in melanoma.";
Cancer Surv. 26:115-132(1996).
42 M.
17870 MW;
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                                                        Query Match
Best Local Similarity 100.0%;
Matches 125; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 395:237-243(1998).
                  167 AA;
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Hayashi N., Sugimoto Y., Tsuchiya E., Ogawa M., Nakamura Y.; "Somatic mutations of the MTS (multiple tumor suppressor) 1/CDK41 (cyclin-dependent kinase-4 inhibitor) gene in human primary non-small cell lung carcinomas.";
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                                                                                                                                                                                                                                                                                                                                     VARIANTS MELANOMA THR-49; SER-71; PRO-87; TRP-101; ASP-126 & THR-148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Okamoto A., Hussain S.P., Hagiwara K., Spillare E.A., Rusin M.R., Demetrick D.J., Serrano M., Hannon G.J., Shiseki M., Zariwala M., Bennett W.P., Forrester K., Gerwin B., Beach D.H., Harris C.C.; Mutations in the pi6INK4/MISI/CDKN2, pi5INK4B/MIS2, and pl8 genes primary and metastatic lung cancer."; Cancer Res. 55:1448-1451(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The MTS1 gene is frequently mutated in primary human esophageal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zhou X., Tarmin L., Yin J., Jiang H.-Y., Suzuki H., Rhyu M.-G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fitzgerald M.G., Harkin D.P., Silva-Arrieta S., Macdonald D.J., Lucchina L.C., Unsal H., O'Neill E., Koh J., Finkelstein D.M., Isselbacher K.J., Sober A.J., Haber D.A.; Prevalence of germ-line mutations in p16, p19ARF, and CDK4 in familial melanoma: analysis of a clinic-based population."; Proc. Natl. Acad. Sci. U.S.A. 93:8541-8545(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ranade K., Hussussian C.J., Sikorski R.S., Varmus H.E.,
Goldstein A.M., Tucker M.A., Serrano M., Hannon G.J., Beach D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Walker G.J., Hussussian C.J., Flores J.F., Glendening J.M., Haluska F.G., Dracopoli N.C., Rayward N.K., Fountain J.W.; "Mutations of the CDKNZ/P16INK4 gene in Australian melanoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VARIANTS SQUAMOUS CELL CARCINOMA (SCCA) SER-127 AND CYS-144 MEDLINE; 95060835.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mutations associated with familial melanoma impair pl6INK4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Harland M., Meloni R., Gruis N., Pinney E., Brookes S., Sp
Frischauf A.-M., Bataille V., Peters G., Cuzick J., Selby
                                                                                                                                                                                                                                                         Biochem. Biophys. Res. Commun. 202:1426-1430(1994).
VARIANTS NON-SMALL CELL LUNG CARCINOMAS (NSCLC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fum. Mol. Genet. 4:1845-1852(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VARIANTS FAMILIAL MELANOMA. MEDLINE; 98087572.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oncogene 9:3737-3741(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genet. 8:15-21(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE; 96121580.
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CDN5_HUMAN
P42772;
          VARIANT
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                                                                                                                                                                                                                                                                                    -1 - SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 X ANK MOTIF REPEATS.
ANK MOTIF 1 (INCOMPLETE).
ANK MOTIF 2.
ANK MOTIF 3.
ANK MOTIF 4.
D > E (IN A BILIARY TRACT TUMOR).
FTICA-VAR.001408.
L -> P (IN A BILIARY TRACT TUMOR) A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /FTIG-VAR_001409.
A -> P (IN A LUNG TUMOR AND MELANOMA).
/FTIG-VAR_001410.
A -> S (IN A BILIARY TRACT TUMOR).
/FTIG-VAR_001411.
G -> D (IN A PANCREAS TUMOR).
/FTIG-VAR_001412.
R -> C (IN MELANOMA).
                                                                                   VARIANT PANCREATIC CARCINOMA CYS-146.
MOSKALUK C.A., HTUDAR R.H., Liderman A., Smyrk T., Fusaro L.,
Fusaro R., Lynch H.T., Kern S.E.;
"Novel germline pl6INK4 allele (Aspl45Cys) in a family with multiple
                                                                                                                                                           Soufir N., Avril M.-F., Chompret A., Demenals F., Bombled J.,
Spatz A., Stoppa-Lyonnet D., Benard J., Bressac-De Paillerets B.;
Hum. Mol. Genet. 7:941-941(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Repeat; ANK repeat; Disease mutation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /FIIG-VAR_001414.
E -> D (IN A BILIARY TRACT TUMOR).
FIIG-VAR_001415.
L -> P (IN FAMILIAL MELANOMA).
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                                                                                                                                                                                                                                                                                                         -1- SIMILARITY: CONTAINS 4 ANK REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL, U12820; AAB60645.1; -
EMBL, U12818; AAB60645.1; JOINED.
EMBL; U12819; AAB60645.1; JOINED.
EMBL; S69804; AAD14048.1; -
EMBL; X94154; CAA63870.1; -
PDB: 1B17; 16-FEB-99.
families in France.";
Hum. Mol. Genet. 7:209-216(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; L27211; AAA92554.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cell cycle; Anti-oncogene; 1
Polymorphism; 3D-structure.
                                                                                                                                        Hum. Mutat. 12:70-70(1998).
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                                                                                                                              pancreatic carcinomas.
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DOMAIN
REPEAT
REPEAT
REPEAT
                               ERRATUM
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Matera G.A., Xiong Y.;
"Growth suppression by p18, a p16INK4/MTS1- and p14INK4B/MTS2-related
CDK6 inhibitor, correlates with wild-type pRb function.";
Genes Dev. 8:2939-2952(1994).
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Science 264:436-440(1994).
                                                                                                                                                                                                                                                            1 MAMGNVHVAALLLNYGADSNCEDPTTFSRPVHDAAREGFLDTLVVLHGSGARLDVRDAWG 60
                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 94359613.
Hannon G.J., Beach D.;
"pl5INK4B is a potential effector of TGF-beta-induced cell cycle
/FTId=VAR_001416.
E -> D (IN A BILIARY TRACT TUMOR).
                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-CT-1996 (Rel. 34, Last annotation update)
CYCLIN-DEPENDENT KINASE 4 INHIBITOR B (P14-INK4B) (P15-INK4B)
CDENIPLE TUMOR SUPPRESSOR 2) (MTS2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE; 94204645.
Kamb A., Gruis N.A., Weaver-Feldhaus J., Liu Q., Harshman K.,
Tavtigian S.V., Stockert E., Day R.S. III, Johnson B.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                              Length 156;
                                                                                                                                           Score 473; DB 1; Length 156
Pred. No. 3.49e-86;
14; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VARIANTS LUNG ADENOCARCINOMA GLU-47 AND VAL-50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            138 AA.
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                                                                     Note: remainder of annotations omitted.
                                                                                                                                                                                                                                                                                                                                                                            112 RLPVDLAEELGHRDVARYLRAAA 134
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RLPLDLAQERGHQDIVRYLRSAG 83
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                                                                                                                                        53.0%;
llarity 73.5%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                           33
                                                                                                             Query Match
Best Local Similarity '61; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE; 95095079.
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the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -:- SUBUNIT: HETERODIMER OF P14 WITH CDK4 (BY SIMILARITY).
-:- TISSUE SPECTIFICITY: EXPRESSED UBIOUITOUSLY.
-:- INDUCTION: BY TGF-BETA.
-:- SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alterations in murine primary T-cell lymphomas.";
Oncogene 14:1361-1370(1997).
-!- FUNCTION: INTERACTS STRONGLY WITH CDK4 AND CDK6. POTENT INHIBITOR.
POTENTIAL EFFECTOR OF TGF-BETA INDUCED CELL CYCLE ARREST (BY
                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
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STRAIN=C57BL/61 X DBA;
MEDLINE; 9732242.
Malumbres M., de Castro I., Santos J., Melendez B., Mangues R.,
Serrano M., Pellicer A., Fernandez-Piqueras J.;
"Inactivation of the cyclin-dependent kinase inhibitor pl5INK4b ideletion and de novo methylation with independence of p16INK4a
                                                                                                                                                   Repeat; ANK repeat; Disease mutation.
2 X ANK MOTIF REPEATS.
ANK MOTIF 1 (INCOMPLETE).
ANK MOTIF 2.
                                                                                                                                                                                                                  G -> E (IN LUNG ADENOCARCINOMA).
/FIId-VAR_001488.
A -> V (IN LUNG ADENOCARCINOMA).
/FIId-VAR_001489.
SA -> TP (IN REF. 2).
MISSING (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-UTL-1998 (Rel. 36, Last annotation update)
CYCLIN-DEPENDENT KINASE 4 INHIBITOR B (P14-INK4B).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                             Length 138;
                                                                                                                                                                                                                                                                                                                                                            Score 472; DB 1; Length 138;
Pred. No. 6.14e-86;
13; Mismatches 8; Indels
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0D6FFBDFA6FEAD21 CRC64;
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                                                                                                                                                                                                                                                                                21 S7
23 M1
34 Q1
14722 MW;
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RLPLDLAQERGHQDIVRYLRSA 82
                                                                                           EMBL; U17075; AAC50075.1; -. EMBL; L36844; AAA50282.1; -. EMBL; S69805; AAD14049.1; -.
                                                                                                                                                                                                                                                                                                                                                          Query Match 52.9%;
Best Local Similarity 74.4%;
Matches 61; Conservative
                                                                                                                                                          cycle; Anti-oncogene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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103
47
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23
32
138 AA;
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P55271;
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CONFLICT
CONFLICT
SEQUENCE
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-!- SIMILARITY: CONTAINS 2 ANK REPEATS.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -:- SUBUNTT: HÉPERODIMER OF P14 WITH CDK4.
-:- ALTERNATIVE PRODUCTS: A SHORTER FORM MAY ARISE BY ALTERNATIVE
INITIATION CODONS IN THE SAME READING FRAME.
-:- TISSUE SPECIFICITY: EXPRESSION ABUNDANT IN LUNG, LESS ABUNDANT IN
TESTIS, BARELY DETECRABLE IN LIVER, AND NOT DETECTABLE IN NEONATAL
KIDNEY, ADULT KIDNEY, BRAIN, HEART, OR SPLEEN.
-:- SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           **Rapek D.F., Serrano M., Beach D., Trono D., Walker C.L.;

"Association of rat pl5INK4B/pl6INK4 deletions with monosomy 5 in
kidney epithelial cell lines but not primary renal tumors.";

Cancer Res. 55:1607-1612(1995).

-i- FUNCTION: INTERACTS STRONGLY WITH CDK4 AND CDK6. POTENT INHIBITOR.

POTENTIAL EFFECTOR OF TGF-BETA INDUCED CELL CYCLE ARREST (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                      46 MANGSAQVAELLILHGAEPNCADPATLIRPVHDAAREGFLDTLVVLHRAGARLDVCDAWG 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
CYCLIN-DEPENDENT KINASE 4 INHIBITOR B (P14-INK4B) (P15-INK4B)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hino O., Kobayashi E., Hirayama Y., Kobayashi T., Kubo Y., Tsuchiya H., Kikuchi Y., Mitani H.; "Molecular genetic basis of renal carcinogenesis in the Eker : model of tuberous sclerosis (Tsc2)."; Mol. Carcinog. 14:23-27(1995).
                                                                                                                                                                                                                                                                                                                                                             Length 130;
                                                                                                                                                                                                                                                                                                                                                           Score 461; DB 1; Length 130
Pred. No. 3.05e-83;
14; Mismatches 8; Indels
                                                                                                                                                                                                                                           Cell cycle; Anti-oncogene; Repeat; ANK repeat.

DOMAIN

S 95

2 X ANK MOTIF REPEATS.

REPEAT

5 31

ANK MOTIF 1 (INCOMPLETE).
                                                                                                                                                                                                                                                                                                                        13788 MW; 7AAD60FF552BCFF9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              130 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -! - SIMILARITY: CONTAINS 2 ANK REPEATS.
                                                                                                                                                                                                                                                                                                      ANK MOTIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                  EMBL; U66085; AAB39833.1; -. EMBL; U66084; AAB39833.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 106 RLPVDLAEEQGHRDIARYLHAA 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 RIPLDLAQERGHQDIVRYLRSA 82
                                                                                                                                                                                                                                                                                                                                                           51.7%;
ilarity 73.2%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [2]
SEQUENCE OF 46-86 FROM N.A.
                                                                                                                                                                                                       MGD; MGI:104737; CDKNZB.
PFAM; PF00023; ank; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     130 AA;
                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
les 60; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE; 96001392.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE; 95228036.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDKN2B OR INK4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LT 5
CDN5_RAT
P55272;
                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                               Query Match
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Matches
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78
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the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                          or send au.

EMBL; S79760; AAB3360.1; -.

EMBL; S77734; CAB33639.1; -.

PFAM; PF00023; ank; 3.

Cell cycle; Anti-oncogene; Repeat; ANK repeat; Alternative initiation.

Coll cycle; Anti-oncogene; Repeat; ANK repeat; Alternative initiation.

CYCLIN-DEPENDENT KINASE 4 INHIBITOR B,

LONG FORM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -1- SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Repeat; ANK repeat; Alternative initiation. 4 x ANK MOTIF REPEATS.
ANK MOTIF 1 (INCOMPLETE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46 MMGSAQVAELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLMVLHKAGARLDVCDAWG 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
CYCLIN-DEPENDENT KINASE 4 INHIBITOR A (CDK4I) (P16-INK4)
(TUMOR SUPPRESSOR CDKN2A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sherburn T.E., Gale J.M., Ley R.D.;
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: INTERACTS STRONGLY WITH CDR4 AND CDK6. INHIBITS THEIR
ABILITY TO INTERACT WITH CYCLINS D. COULD ACT AS A NEGATIVE
REGULATOR OF THE PROLIFERATION OF NORMAL CELLS (BY SIMILARITY).

-!- SUBUNIT: HETERODIMER WITH CDR4 OR CDK6 (BY SIMILARITY).

-!- ALTERNATIVE PRODUCTS: A SHORTER FORM MAY ARISE BY ALTERNATIVE
INITIATION CODONS IN THE SAME READING FRAME.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Monodelphis domestica (Short-tailed grey opossum).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Metatheria; Didelphimorphia; Didelphidae; Monodelphis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 457; DB 1; Length 130;
Pred. No. 2.90e-82;
15; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                    46 46 FOR THE SHORT FORM.
5 95 2 X ANK MOTIF REPEATS.
5 31 ANK MOTIF 1 (INCOMPLETE).
65 95 ANK MOTIF 2.
130 AA: 13748 MW. AC45B21FA69FAD92 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          171 AA.
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-1- SIMILARITY: CONTAINS 4 ANK REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     106 RLPVDLAEEQGHRDIARYLHAA 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |||:|||:||:||:|
61 RLPLDLAQERGHQDIVRYLRSA 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cell cycle; Anti-oncogene;
DOMAIN 46 169
REPEAT 46 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 51.2%;
Best Local Similarity 72.0%;
Matches 59; Conservative
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CDN2_MONDO
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DOMAIN
REPEAT
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MEDILINE; 96121373.
OKUGA T., Hiral H., Valentine V.A., Shurtleff S.A., Kidd V.J.,
Lahti J.M., Sherr C.J., Downing J.R.;
"Molecular cloining, expression pattern, and chromosomal localization
"Molecular cloining, expression pattern, and chromosomal incalization of human CDKNZD/INK4d, an inhibitor of cyclin D-dependent Kinases.";
Genomics 29:623-630(1995).
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Baumgartner R., Fernandez-Catalan C., Winoto A., Huber R., Engh R.A.,
                                                                                                                                                                                                                                                                                                                                    Guan K.L., Jenkins C.W., Li Y., O'Reefe C.L., Noh S., Wu X., Zariwala M., Matera A.G., Xiong Y.; "Isolation and characterization of pl9INK4G, a pl6-related inhibitor specific to CPRS and CMA.".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Russo A.A., Tong L., Lee J.O., Jeffrey P.D., Pavletton N.P.; "Structural basis for inhibition of the cyclin-dependent kinase Cdk6 by the tumour suppressor pl6INK4a."; Nature 395:237-243(1998).
                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Newton Bishop J.A., Harland M., Bennett D.C., Bataille V.,
Goldstein A.M., Tucker M.A., Ponder B.A.J., Cuzick J., Selby P.,
Bishop D.T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Mutation testing in melanoma families: INK4A, CDK4 and INK4D.";
Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chan F.K.M., Zhang J., Cheng L., Shapiro D.N., Winoto A.; "Identification of human and mouse pl9, a novel CDK4 and CDK6 inhibitor with homology to pl6ink4 "; movel cell. Biol. 15:2682-2688(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhin!; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF COMPLEX WITH CDK6
                                                                                                                                                                                Length 171;
                                                                                                                                                    Score 434; DB 1; Length LAL. Pred. No. 1.19e-76;
109 ANK MOTIF 2.
143 ANK MOTIF 3.
169 ANK MOTIF 3.
34 MISSING (IN SHORT ISOFORM).
18707 MW, 694264F5D0F4F6CC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 7 2 2EUNAN STANDARD; PRT; 166 AA. P5573; 013102; 01-0CT-1996 (Rel. 34, Created) 01-0CT-1996 (Rel. 34, Last sequence update) 15-0L-1999 (Rel. 38, Last annotation update) CYCLIN-DEPENDENT KINASE 4 INHIBITOR D (P19-INK4D).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      specific to CDK6 and CDK4.";
Mol. Biol. Cell 7:57-70(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                        146 RLPVDLAEEQGHHLVVAYLR 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                       48.7%;
71.3%;
                                                                                                                                                                                                                                              57; Conservative
                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                     171 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. TISSUE-THYMUS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE; 95257949.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE; 96362662.
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                                                                                                                                                        Nature 389:999-1003(1997).
-!- FUNCTION: INTERACTS STRONGLY WITH CDK4 AND CDK6.
-!- SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             49 MAFGSPAVALELLKQGASPNVQDASG-TSPVHDAARTGFLDTLKVLVEHGADVNALDSTG 107
                                                                                                                  Laue E.D.; "Structure of the cyclin-dependent kinase inhibitor pi9Ink4d.";
                                                                        Luh F.Y., Archer S.J., Domaille P.J., Smith B.O., Owen D., Brotherton D.H., Raine A.R., Xu X., Brizuela L., Brenner S.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Repeat; ANK repeat; 3D-structure.
4 X ANK MOTIF REPEATS.
ANK MOTIF 1.
ANK MOTIF 2.
ANK MOTIF 3.
ANK MOTIF 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 218; DB 1; Length 166;
Pred. No. 3.88e-26;
13; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A -> P (IN REF. 2).
9E74F5C23B7EBCB2 CRC64;
                                                                                                                                                                                                                                    -1- SIMILARITY: CONTAINS 4 ANK REPEATS.
    Mol. Cell. Biol. 15:2682-2688(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KINASE 4 INHIBITOR C) (P18-INK4C)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17 17 17 19 166 AA; 17894 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U19597; AAC52194.1; -. EMBL; U20497; AAA85437.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 24.4%;
Best Local Similarity 48.1%;
Matches 38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cell cycle; Anti-oncogene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                PDB; 1AP7; 16-SEP-98.
MGD; MGI:105387; CDKN2D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PFAM; PF00023; ank; 3.
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STRAIN-C57BL KAPLAN;
MEDLINE; 95257948.
                                          STRUCTURE BY NMR. MEDLINE; 98013176.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42
73
105
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                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                              CYCLIN-DEPENDENT KINASE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Gaps
Holak T.A.; Structure of human cyclin-dependent kinase inhibitor p19(INK4d): Structure of human cyclin-repeat-containing structures and implications for the dysfunction of tumor suppressor p16(INK4a)."; Structure 6:1279-1290(1998).
-!- FUNCTION: INTERACTS STRONGIN WITH CDK4 AND CDK6.
-!- SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hirai H., Roussel M.F., Kato J.-Y., Ashmun R.A., Sherr C.J.; hovel Inra proteins, p19 and p18, are specific inhibitors of the cyclin D-dependent kinases CDK4 and CDK6."; Mol. Cell. Biol. 15:2672-2681(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chan F.K.M., Zhang J., Cheng L., Shapiro D.N., Winoto A.; "Identification of human and mouse pl9, a novel CDK4 and CDK6 inhibitor with homology to pi6ink4.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       :; ANK repeat; 3D-structure.
ANK MOTIF REPEATS.
MOTIF 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 1.91e-29;
15; Mismatches 29; Indels
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2FACD11CF56340DC CRC64;
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104 AN
137 AN
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EMBL; U40343; AAB18139.1; -.
EMBL; U20498; AAA85436.1; -.
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Best Local Similarity 46.5%;
Matches 40; Conservative
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STRAIN-C57BL KAPLAN;
MEDLINE; 95257948.
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105 1
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Hiral H., Roussel M.F., Kato J.-Y., Ashmun R.A., Sherr C.J.;
"Novel INK4 proteins, p19 and p18, are specific inhibitors of the
cyclin D-dependent kinases CDK4 and CDK6.";
Mol. Cell. Biol. 15.2672-2681(1995).
-!- FUNCTION: INTERACTS STRONGLY WITH CDK6, WEAKLY WITH CDK4. INHIBITS
CELL GROWTH AND PROLIFERATION WITH A CORRELATED DEPENDENCE ON
1 MAMGNVHVAALLLINYGADSNCEDPTTFSRPVHDAAREGFLDTLVVLHGSGARLDVRDAWG 60
                                                                                                                                                                                                                                                                                                                        CDN6_MOUSE STANDARD; PRT; 168 AA.
060772;
01-NOV-1997 (Rel. 35, Created)
15-DEC-1998 (Rel. 37, Last annotation update)
CYCLIN-DEPENDENT KINASE 6 INHIBITOR (P18-INK6) (CYCLIN-DEPENDENT
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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 SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE
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                                                                                                                                                                                                                                                                                                                                         45 MKLGNPEIARRLLLR-GANPNLKDGTGFA-VIHDAARAGFLDTVQALLEFQADVNIEDNE 102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
CYCLIN-DEPENDENT KINASE 6 INHIBITOR (P18-INK6) (CYCLIN-DEPENDENT
KINASE 4 INHIBITOR C) (P18-INK4C).
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Lapolite J., Lachance Y., Labrie Y., Labrie C.;
"A p18 mutant defective in CDK6 binding in human breast cancer
cella.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                      Score 198; DB 1; Length 168;
Pred. No. 8.29e-22;
18; Mismatches 29; Indels
                                                                                                                                  EMBL; U19596; AACDALL

MGD1:05388; CDKNZC.

( FFMA; PF00023; ank; 3.

A Call cycle; Repeat; ANK repeat.

T DOMAIN 5 135 AK MOTIF 1.

FT REPEAT 5 36 ANK MOTIF 1.

FT REPEAT 37 68 ANK MOTIF 2.

A SANK MOTIF 2.

A SANK MOTIF 2.

A SANK MOTIF 2.

A SANK MOTIF 3.
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                          -1- SIMILARITY: CONTAINS 4 ANK REPEATS.
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60 GRLPLDLAQERGHQDIVRYL-RSAGCSL 86
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Best Local Similarity 42.0%;
Matches 37; Conservative
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MEDLINE; 98300299.
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                                                                                                                                                                                                                                                                          "THICK SUPPRESSOR INK4: determination of the solution structure of p18INK4C and demonstration of the functional significance of loops in p18INK4C and p16INK4A.";

BLOCHAMISLY 38:2930-294.";

-1- FUNCTION: INTERACTS STRONGLY WITH CDK6, WEAKLY WITH CDK4. INHIBITS CELL GROWTH AND PROLIFERATION WITH A CORRELATED DEPENDENCE ON ENDOGROUS RETINOBLASTOMA PROTEIN RB.
-1- SUBUNIT: HETERODIMER OF P18 WITH CDK6.
-1- SUBUNIT: HETERODIMER OF P18 WITH CDK6.
-1- TISSUE SPECIFICITY: HIGHEST LEVELS FOUND IN SKELETAL MUSCLE. ALSO FOUND IN PANCREAS AND HEART.
-1- DISEASE: CDKN2C MUTATIONS ARE INVOLVED IN TUMOR FORMATION.
-1- SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE
Venkataramani R., Swaminathan K., Marmorstein R.; "Crystal structure of the CDK4/6 inhibitory protein plBINK4c provides insights into ankyrin-like repeat structure/function and tumor-derived pl6inK mutations."; Nat. Struct. Biol. 5:74-81(1998).
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                                                                                                                                         STRUCTURE BY NMR.
MEDLINE; 99175088.
Li J., Byson I.-J.L., Ericson K., Poi M.-J., O'Maille P., Selby T.,
Isai M.-D.;
Tsai M.-D.;
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Pred. No. 9.66e-21;
13; Mismatches 28; Indels
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15-UUL-1999 (Rel. 38, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 1 PRECURSOR.
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EMBL; AF041250; AAC39783.1; -.
EMBL; AF041249; AAC39783.1; -.
PDB; 11HB; 13-JAN-99.
PDB; 1BU9; PRELIMINARY.
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DR PRINTS; PRO01010; EGEBLOOD.

DR PROSITE; PS00010; ASX_HYDROXYL; 22.

DR PROSITE; PS001010; ASX_HYDROXYL; 22.

DR PROSITE; PS00108; EGF_1; 35.

DR PROSITE; PS00108; EGF_2; 26.

DR PRAM; PP00002; EGF_1; 36.

DR PFAM; PF00002; EGF_1; 36.

ET SIGNAL

FT DOMAIN 1741 2531 CVPTCTIAL.

THANKSMEM 1724 1746 POTENTIAL.

THE DOMAIN 1747 2531 CVPTCTIAL.

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CYTOPLASMIC (POTENTIAL).

EGF-LIKE 1.

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EGF-LIKE 4.

EGF-LIKE 4.

EGF-LIKE 6.

EGF-LIKE 6.

EGF-LIKE 9.

EGF-LIKE 10.

EGF-LIKE 11.

EGF-LIKE 11.

EGF-LIKE 11.

EGF-LIKE 12.

EGF-LIKE 13.

EGF-LIKE 14.

EGF-LIKE 14.

EGF-LIKE 17.

EGF-LIKE 17.

EGF-LIKE 17.

EGF-LIKE 18.

EGF-LIKE 19.

EGF-LIKE 19
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(POTENTIAL).
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DEVELOPMENTAL STAGE: IN THE EMBRYO, HIGHEST LEVELS OCCUR BETWEEN
DAYS 12 AND 14 AND DECREASE RAPIDLY TO MUCH LOWER LEVELS IN THE
                                                                                                                                                                                                                                                                                            Weinmaster G.;
Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: REQUIRED FOR THE CORRECT DIFFERENTIATION OF A NUMBER
                                         Mammalia;
Rattus.
                                                                                                                                                             Weinmaster G., Roberts V.J., Lemke G.;
"A homolog of Drosophila Notch expressed during mammalian development.";
bevelopment 113:199-205(1991).
[2]
REVISIONS TO 1652-1653.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: HIGH, WITH OTHER NOTCH-TYPE PROTEINS. SIMILARITY: CONTAINS 36 EGF-LIFE DOMAINS. SIMILARITY: CONTAINS 3 LIN/NOTCH REPEATS. SIMILARITY: CONTAINS 6 ANK REPEATS.
                     Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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TISSUE-SCHWANN CELL;
MEDLINE; 92111383.
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RAY SELISEN L.W., Blid J., West D.C., Soreng A.L., Reynolds T.C.,

RAY SELISEN L.W., Blid J., West D.C., Soreng A.L., Reynolds T.C.,

Smith S.D., Sklar J.;

RITAN-1, the human homolog of the Drosophila notch gene, is broken by

RT TAN-1, the human homolog of the Drosophila notch gene, is broken by

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CYTOPLASMIC (POTENTIAL).

EGF-LIKE 1.

EGF-LIKE 2.

EGF-LIKE 3.

EGF-LIKE 5.

CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 6.

EGF-LIKE 1.

EGF-LIKE 2.

EGF-LIKE 2.
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REMEL; M73980; AAA60614.1; -

REMEL; M73980; AAA60614.1; -

REMEL; M73980; ASX_HYDROXYL; 20.

REPROSITE; PS01010; ASX_HYDROXYL; 20.

REPROSITE; PS010185; EGF_2; 26.

REPROSITE; PS010187; EGF_CA; 18.

REPROSITE; PS01008; EGF; 36.

REPROSITE; PS01008; EGF; 36.

REPROSITE; PS01008; EGF; 36.

REPROSITE; PS01008; EGF; 36.

REPROSITE; PS010180; Repeat; Repeat; EGF-11Ke domain; PFAM; PF00008; October 1.

Transmembrane; Signal; Glycoprotein.

Transmembrane; Signal; Glycoprotein.

Transmembrane; Signal; Glycoprotein.

Transmembrane; Signal; EFFRACELLULAR (POTENTIAL).

TRANSMEM 1737 1736 EXTRACELLULAR (POTENTIAL).

TRANSMEM 1737 1758 >2444 CYTOPLASMIC (POTENTIAL).
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NEUROGENIC LOCUS NOTCH PROTEIN HOMOLOG 1.
EXTRACELLULAR (POTENTIAL).
                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Mammalia,
Eutheria, Primates, Catarrhini, Hominidae, Homo.
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P46331;
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 33, Last sequence update)
01-REB-1996 (Rel. 33, Last annotation update)
01-FEB-1996 (Rel. 33, Last annotation update)
ABROGGENIC LOCUS NOTCH PROTEIN HOMOLOG 1 PRECURSOR (TRANSLOCATION-NOTCH OR TAN1.
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Pred. No. 4.22e-13;
12; Mismatches 31; Indels
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    Query Match
Best Local Similarity 42.9%;
Matches 33; Conservative
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   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PURDEGELIAL LOCUS NOTCH HOMOLOG PROTEIN 1. EXTRACELLULAR (POTENTIAL).

36 X EGF-TYPE REPEATS.

36 X EGF-TYPE REPEATS.

36 Y EGF-TYPE REPEATS.

36 Y EGF-LIKE 1.

37 EGF-LIKE 2.

38 EGF-LIKE 3.

38 EGF-LIKE 4.

39 EGF-LIKE 6.

39 EGF-LIKE 6.

30 EGF-LIKE 7.

31 EGF-LIKE 6.

32 EGF-LIKE 9.

33 EGF-LIKE 10.

34 EGF-LIKE 11.

35 EGF-LIKE 11.

36 EGF-LIKE 11.

36 EGF-LIKE 12.

37 EGF-LIKE 13.

38 EGF-LIKE 13.

39 EGF-LIKE 13.

30 EGF-LIKE 13.

30 EGF-LIKE 14.

31 EGF-LIKE 15.

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46 EGF-LIKE 15.

47 EGF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Differentiation: Neurogenesis; Repeat; ANK repeat; EGF-like domain; Transmembrane; Signal; Glycoprotein.

SIGNAL 18 19 2531 NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 19 1725 EXTRACELLULAR (POTENTIAL).

TRANSMEM 1726 746 POTENTIAL.

DOMAIN 1747 2531 CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MGD; MCI-97863; MOTCH1.
PRINTS; PRO0010; EGFBLOOD.
PROSITE; PS00010; ASX_HYDROXIL; 22.
PROSITE; PS001018; EGF_2; 34.
PROSITE; PS01186; EGF_2; 27.
PROSITE; PS01187; EGF_CA; 21.
PFAM; PF00008; EGF; 35.
PFAM; PF00008; EGF; 35.
PFAM; PF00066; notch; 3.
                                                                                                                                                          [2]
SEQUENCE OF 1551-2170 FROM N.A.
TISSUB-EMBXYO;
MEDLINE; 93048835.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; 211886; CAA77941.1; -. HSSP; P00740; 11XA.
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MEDLINE; 93194170.
                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EGF-LIKE 7.

EGF-LIKE 8. CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 10. CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 11. CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 12. CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 13. CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 13. CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 14. CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 15. CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 16. CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 16. CALCIUM-BINDING (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                       Differentiation; Neurogenesis; Repeat; EGF-like domain; Transmembrane;
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STRAIN=ICR X SWISS WEBSTER;
MEDLINE; 95001556.
Landelli M., Dalstrand J., Lendahl U.;
The novel Notch homologue mouse Notch 3 lacks specific epidermal growth factor-repeats and is expressed in proliferating
                                                       Mech. Dev. 46:123-136(1994).

-1- FUNCTION: NOTCH 1, 2 AND 3 PLAY A COMBINATIONAL ROLE DURING VARIOUS CELL FATE DESIGNORS AND MORPHOLOGICAL MOVEMENTS IN T DEVELOPING CNS AND PROBABLY OTHER REGIONS OF THE EMBRYO.

-1- TISSUE SPECIFICITY: PROLIFERATING NEUROEPITHELIUM.

-1- DEVELOPMENTAL STAGE: CNS DEVELOPENT.

-1- SIMILARITY: CONTAINS 34 EGF-LIKE DOMAINS.

-1- SIMILARITY: CONTAINS 3 LIN/MOTCH REPEATS.

-1- SIMILARITY: CONTAINS 6 CDC10/SWI6 REPEATS.
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CALCIUM-BINDING
CALCIUM-BINDING
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CYTOPLASMIC.
34 X BGF-TYPE REPEATS.
3 X LIN/NOTCH REPEATS.
6 X CDC10/SW16 REPEATS.
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EGF-LIKE 3.
EGF-LIKE 4,
EGF-LIKE 5.
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BGF-LIKE
BGF-LIKE
BGF-LIKE
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BGF-LIKE
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PRINTS; PRO0010; EGFBLOOD.
PROSITE; PS00010; BGZ_HT33.
PROSITE; PS01186; EGF_1; 33.
PROSITE; PS01186; EGF_2; 27.
PROSITE; PS01187; EGF_CA: 17.
PPAM; PF00008; EGF; 34.
PFAM; PF00003; ank; 6.
PFAM; PF00066; notch; 3.
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HSSP; P00740; 11XA.
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 2531;
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Pred. No. 1.03e-11;
15; Mismatches 32; Indels
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01-NOV-1997 (Rel. 35, Last sequence update)
01-UL-1998 (Rel. 36, Last annotation update)
NEUROGENIC LOCUS NOTCH 3 PROTEIN.
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  2086 PRDIAGERMHHDIVRLL 2102
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Best Local Similarity 37.7%;
Matches 29; Conservative
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63 PLDLAQERGHQDIVRYL 79
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RESULT 15
ID NOTC_BRARE STANDARD; PRT; 2437 AA.
AC P46530;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE IS-JUL-1998 (Rel. 36, Last annotation update)
DE STANDARD (LOCUS NOTCH HOMOLOG PROTEIN PRECURSOR.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii; CC Cyprinoidea; Cyprinidae; Rasborinae; Danio.
CC Cyprinoidea; Cyprinidae; Rasborinae; Danio.
RP SEQUENCE FROM N.A.
RC TISSUE=EMBRYO;
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Pred. No. 2.53e-11;
14; Mismatches 31; Indels
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   2009 PRDVAQERLHQDIVRLL 2025
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Best Local Similarity 40.3%;
Matches 31; Conservative
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CALCIUM-BINDING (POTENTIAL)
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EGF-LIKE 27,
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EGF-LIKE 33.
EGF-LIKE 33.
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EGF-LIKE 34.
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3 X LIN/NOTCH 2.
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            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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| R EMBL; X69088; CAA48831.1; -
| R HSSP; P00740; IIXA. |
| R SETIN; 2DB-GENEP-990415-173; NOTCH. |
| R PRINTS; PR000009; EGFTGF. |
| R PROSITE; PS00010; ASX_HYDROXYL; 23. |
| R PROSITE; PS001186; EGF_2; 28. |
| R PROSITE; PS001187; EGF_A; 22. |
| R PROSITE; PS001187; EGF_A; 22. |
| R PROSITE; PS001187; EGF_A; 32. |
| R PRAM; PF000066; notch; 3. |
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GEF-LIKE 1.

GGF-LIKE 2.

GGF-LIKE 3.

EGF-LIKE 4.

EGF-LIKE 4.

EGF-LIKE 6.

EGF-LIKE 7.

CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 9.

CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 10.

EGF-LIKE 10.

EGF-LIKE 11.

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EGF-LIKE 12.

EGF-LIKE 13.

CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 13.

EGF-LIKE 14.

EGF-LIKE 14.

EGF-LIKE 15.

CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 15.

CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 15.

CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 16.

CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 19.

CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 20.

CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 21.

CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 22.

EGF-LIKE 23.

CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 24.

EGF-LIKE 25.

EGF-LIKE 27.

EGF-
MEDLINE: 94128602.

A Blerkamp C., Campos-Ortega J.A.;
Blerkamp C., Campos-Ortega J.A.;

A zabrafish homologue of the Drosophila neurogenic gene Notch and its pattern of transcription during early embryogenesis.";

Mech. Dev. 43:87-100(1993).

-1 FUNCITON: IMPLICATED IN CELL FATE SPECIFICATIONS DURING EMBRYO DEVELOPMENT. MAY BE INVOLVED IN THE FORMATION OF THE NEURAL PLATE, NOTOCHORD AND BRAIN VESICLES.

-1 SUBCELLUIAR LOCATION: TYPE I MEMBRANE PROTEIN.

-1 DEVELOPMENTAL STAGE: EXPRESSED IN ALL CELLS IN PREGASTRULATION STAGES. DURING GASTRULATION IS DIFFERENTIALLY EXPRESSED, ACCUMULATING PREDOMINANTLY IN THE PRECHOPING MESODERM AND NOTOCHORD. AT THE END OF GASTRULATION, EXPRESSED ALONG THE ANTERIOR-POSTERIOR AND SASTRULATION, EXPRESSED ALONG THE ANTERIOR-POSTERIOR MESODERM. ALSO PRESENT IN THE DEVELOPING BRAIN AND DIFFERENTIATING MESODERM. ALSO PRESENT IN THE DEVELOPING STAILLARITY: CONTAINS 36 EGF-LIKE DOMAINS.

-1 SIMILARITY: CONTAINS 3 LINVOTCH REPEATS.

-1 SIMILARITY: CONTAINS 6 ANK REPEATS.
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Note: remainder of annotations omitted.

Score 146; DB 1; Length 2437; Pred. No. 3.97e-11; 14; Mismatches 31; Indels 1; Gaps 1; Query Match
Best Local Similarity 40.3%;
Matches 31; Conservative

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Search completed: Thu Jul 20 08:42:34 2000 Job time : 9 secs.

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protein . protein database search, using Smith-Waterman algorithm MPsrch_pp

Thu Jul 20 08:42:52 2000; MasPar time 16.56 Seconds 523.462 Million cell updates/sec Run on:

Tabular output not generated.

>US-09-016-869A-6
(1-125) from US09016869A.pep
892
1 MMMGNVHVAALLLNYGADSN......SFSSSIPRALELRGGSQEQS 125 Title: Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

225878 segs, 69334122 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

sptrembl12
1.sp_archea 2.sp_bacteria 3.sp_fung1 4.sp_human
5.sp_invertebrate 6.sp_mammal 7.sp_mhc 8.sp_organelle
9.sp_bhage 10.sp_plant 11.sp_rodent 12.sp_unclassified
13.sp_vertebrate 14.sp_virus

Mean 41.331; Variance 69.208; scale 0.597 Statistics: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No. Score Match Length DB ID Description Pred.			đ					
100.0 168 11 P97510 CYCLIN DEPENDENT KINAS 99.8 168 11 089088 CYCLIN DEPENDENT KINAS 90.4 113 11 092162 CYCLIN DEPENDENT KINAS 54.7 86 6 09X552 P16/CDKNZA/MTS1 (FRAGM 53.0 115 4 016361 CYCLIN-DEPENDENT KINAS 50.8 86 11 054846 CYCLIN-DEPENDENT KINAS 126.3 124 13 09W618 P13CDKUX. 24.0 58 6 09786 CYCLIN-DEPENDENT KINAS 13 097067 CYCLIN-DEPENDENT KINAS 13 097067 CYCLIN-DEPENDENT KINAS 11 090905 CYCLIN-DEPENDENT KINAS 11 090905 CYCLIN-DEPENDENT KINAS 12 13 097067 CYCLIN-DEPENDENT KINAS 11 001905 CYCLIN-DEPENDENT KINAS 21 12 13 093617 NOTCH PROTEIN HOMOLOG 21 17.2 135 13 093617 NOTCH PROTEIN HOMOLOG 21 17.0 2447 13 093617 NOTCH PROTEIN HOMOLOG 21 17.0 2447 13 093617 NOTCH CRAGMENT). 16 497 14 096796 NOTCH CRAGMENT). 16 6 497 14 096796 NOTCH2 (FRAGMENT). 16 6 497 14 096794 NOTCH2 (FRAGMENT). 16 6 497 14 096794 NOTCH2 (FRAGMENT). 16 6 497 14 096794 NOTCH2 (FRAGMENT).	Result No.	Score	Query Match	Length	DB	А	Description	Pred. No.
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	20	148	16.6	497	7	096794	-	6.99e-11

6.99e-11	6.99e-11	6.99e-11	1.08e-10	1.68e-10	4.02e-10	6.21e-10	5.37e-09	8.23e-09	1.26e-08	1.26e-08	1.26e-08	2.95e-08	4.50e-08	1.04e-07	1.59e-07	1.59e-07	2.41e-07	2.41e-07	2.41e-07	2.41e-07	2.41e-07	2.41e-07	2.41e-07	5.53e-07
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148	148	148	147	146	144	143	138	137		136	136	134	133	131	130	130	129	129	129	129	129	129	129	127
21	22	23	24	25	56	27	28	53	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

Proc. Natl. Acad. Sci. U.S.A. 95:2429-2434(1998).

SEQUENCE OF 1-42 FROM

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STRAIN-CAST/EI, C57BL/6J AND RF/J, MOLF/EI AND MUS MUS CULUGS;
A SANTOS J. MELENDEZ B. PEREZ DE CASTRO I., MALUMBRES M., SERRANO M.,
PELLICER A., FERNANDEZ-PIQUERS J.;
"Comparative analysis of the pi6(INK4a) and pi5(INK4b) DNA sequences
II "Comparative analysis of the pi6(INK4a) and pi5(INK4b) DNA sequences
II mouse inbred strains.";
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
REMBL; ARC04336; AAC08963.1;
REMBL; U66087; AAS00963.1;
REMBL; U66087; AAB39600.1;
REMBL; U66087; AAB39600.1;
REMBL; U66087; AAB39600.1;
REMBL; U77081 AAB39600.1;
REMBL; U770828; AAD00226.1;
REMBL; U77082, AAD00226.1;
REMBL; U77082, AAD00226.1;
REMBL; U77082, AAD00226.1;
REMBL; U77082, AAD00223.1;
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01-NOV-1998 (TrEMBLrel, 08, Created)
01-NOV-1999 (TrEMBLrel, 12, Last sequence update)
01-NOV-1999 (TrEMBLrel, 12, Last annotation update)
01-NOV-1999 (TREMBLEL)

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MEDLINE; 98151529.
ZHANG S., RAMSAY E.S., MOCK B.A.;
"CdknZa, the cyclin-dependent kinase inhibitor encoding pl6INK4a and p19ARF, is a candidate for the plasmacytoma susceptibility locus, Pctrl.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOLOFF E.V., HERZOG C.R., YOU M.; "The 5'-flanking region of the El alpha form of the murine pl6INK4a
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                      GRESSANI K.M., ROLLINS L.A., MILLER M.S.;
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
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[5]
SEQUENCE OF 1-42 FROM N.A.
STRAIN-DBA/2 AND C57BL/6;
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                                                                                                                                                                         SEQUENCE OF 1-11 FROM N.A. STRAIN-ICR SWISS;
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P42771: 1B17.
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                                                                                                                                                                                                                                  MEDLINE; 97128829
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SQEQS 125
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C STRAIN-BALB/CJ AND MUS MUS POSCHIAVINUS;
SEQUENCE OF 1-42 FROM N.A.
SEQUENCE OF 1.42 FROM N.A.
SANTOG J., MELENDEZ B., PEREZ DE CASTRO I., MALUMBRES M., SERRANO M.,
SANTOG J., MELENDEZ-PIQUERAS J.;
T "Comparative analysis of the p16(INK4a) and p15(INK4b) DNA sequences
I "Comparative analysis of the p16(INK4a) and p15(INK4b) DNA sequences
I "Comparative analysis of the p16(INK4a) and p15(INK4b) DNA sequences
I "Comparative analysis of the p16(INK4a) and p15(INK4b) DNA sequences
I "MALS ARCO0051.1; -..
REBL; AF044335; AAC08962.1; -..
REBL; AP04279; AAC08962.1; -..
REBL; U79626; AAD00224.1; -..
REBL; U796279; AAC00051.1; -..
REBL; U79626; AAD00224.1; -..
REBL; U79626; AAD00224.1; -..
REBL; U796279; AAC0023; ARCO023; A
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                                                                                                                                       HERZOG C.R., YOU M.; "Sequence variation and chromosomal mapping of the murine Cdkn2a tumor
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SANTOS J., MELENDEZ B., PEREZ DE CASTRO I., MALUMBRES M., SERRANO M.,
SANTOS J., MELENDEZ B., PEREZ DE CASTRO I., MALUMBRES M., SERRANO M.,
PELLICER A., FERNANDEZ-PIQUERAS J.;
"Comparative analysis of the p16(INK4a) and p15(INK4b) DNA sequences
in mouse inbred strains.",
Submitted (CCT-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; U79634; AAD00236.1; -.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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Pred. No. 5.44e-185;
1; Mismatches 0; Indels
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Last annotation update)
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Q921C2
Q921C2;
Q1C2
Q1C2
Q1-MAY-1999 (TrEMBLrel. 10, C)
Q1-MAY-1999 (TrEMBLrel. 10, Le
Q1-NOV-1999 (TREMBLREL. 10, Le
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Best Local Similarity 99.2%;
Matches 124; Conservative
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                                                                             STRAIN=MA/M4J;
MEDLINE; 97179476.
                                                                                                                                                                                              suppressor gene.";
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2 MMMGNVHVAALLLNYGADSNCEDPTTFSRPVHDAAREGFLDTLVVLHGSGARLDVRDAWG 61

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62 RLPVDLAEERGHRDVARYLRAAA
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016361;
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OKUDA M., CHO K., SETOGUCHI A., MINEHATA K., YAZAWA M., ENDO Y.,
NISHIGAKI K., WATARI T., TSUJIMOTO H., HASEGAWA A.;
"Cloning and chromosomal mapping of the feline genes p16(MTS1/CDKNZA)
and p15(MTS2/CDKNZB).";
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AB010807; BAA33540.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OKUDA M., CHO K., SETOGUCHI A., MINEHATA K., YAZAWA M., ENDO Y., NISHIGAKI K., WATARI T., TSUJIMOTO H., HASEGAWA A.; "Cloning and chromosomal mapping of the feline genes pl6(MTS1/CDKNZA) and pl5(MTS2/CDKNZA)."; Submitted (JAN-1998)."; EMBL, AB010808; BAA33541.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8
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                                                                                                                RLPLDLAQERGHQDIVRYLRSAGCSLCSAGWSLCTAGNVAQTDGHSFSSSTP 113
                                                                                                                                                          61 RLPLDLAQERGHQDIVRYLRSAGCSLCSAGWSLCTAGNVAQTDGHSFSSSTP 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Felis silvestris catus (Cat).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Carnivora; Fissipedia; Felidae; Felis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
P15/MTS2/CAN2B (FRAGMENT).
Felis silvestris catus (Cat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Carnivora; Fissipedia; Felidae; Felis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 492; DB 6; Length 102;
Pred. No. 7.62e-88;
11; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 488; DB 6; Length 86;
Pred. No. 6.86e-87;
13; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               102 102 102 102 10824 MW; 8C3094E9 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         86 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86 AA; 9340 MW; 8C5D01A0 CRC32;
                                                                                                                                                                                                                                                                                                                                                               102
                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55.2%;
79.0%;
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Best Local Similarity 75.9%;
Matches 63; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P16/CDKN2A/MTS1 (FRAGMENT)
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                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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Best Local Similarity
Matches 64; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
TISSUE-PBMC;
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SEQUENCE
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09XS52
09XS52;
                                                                                                                                                                                                                                                                                                                                                                                            09XS51;
                                                                                                                                                                                                                                                                                                                             T 4
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SANTOS J., MELENDEZ B., PEREZ DE CASTRO I., MALUMBRES M., SERRANO M.,
PELLICER A., FERNANDEZ-PIQUERAS J.;
"Comparative analysis of the p16(INK4a) and p15(INK4b) DNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11 MMGSARVAELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWG 70
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Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ë
                                                                                                                                                                                                                                                                                                                                                               Mammalla;
                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE; 95330726.
STONE S., JIANG P., DAYANANTH P., TAVTIGIAN S.V., KATCHER H.,
PARNY D., PETERS G., KAMB A.;
"Complex structure and regulation of the P16 (MTS1) locus.";
Cancer Res. 55:2988-2994(1995).
EMBL; S78535; AAC60650.1; --
HSSP; P42771; 1B17.
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Pred. No. 1.80e-80;
14; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 473; DB 4; Length 115
Pred. No. 2.55e-83;
14; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  in mouse inbred strains.";
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; 079637; AAD00237.1; -.
HSSP; P42771; 1BI7.
Kinase; Cyclin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0921C1 PRELIMINARY; PRT; 86 AA.
0921C1;
01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MOV-1999 (TrEMBLrel. 12, Last annotation update)
CYCLIN-DEPENDENT KINASE INHIBITOR PROTEIN (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                               01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
CELL CYCLE NEGATIVE REGULATOR BETA FORM (FRAGMENT).
P16/MTSI/CDKN2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             115 AA; 12334 MW; F5BEF54B CRC32;
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                                                                                                                                                       115 AA
                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus spretus (Western wild mouse).
84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71 RLPVDLAEELGHRDVARYLRAAA 93
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61 RLPLDLAQERGHQDIVRYLRSAG
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73.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Match 53.0%;
Local Similarity 73.5%;
hes 61; Conservative
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Matches 60; Conservative
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ACCOSON

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SEQUENCE FROM N.A.
STRAIN-JP 163 A; IISSUE-MUSCLE;
MEDLINE; 97075115.
NAIRN R.S., KAZIANIS S., MCENTIRE B.B., DELLA COLETTA L., WALTER R.B.,
MORIZOT D.C.;
                                                                                                                                                                                                                                                                                                                                          Xiphophorus maculatus (Southern platyfish).
Eukaryota, Metazoa, Chordata; Craniata; Vertebrata; Actinopterygil;
Neopterygil; Teleostei; Euteleostei; Acanthopterygil; Atherinomorpha;
Cyptinodontiformes; Cyptinodontoldei; Poeciliidae; Xiphophorus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43 MMMGSSEVARLLLTRGADPNVTDKSTGATPLHDAARTGFLDTVQLLVKAGADPQARDKDN 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RIEDER S., CHECA-CORTES M.L., JOERG H., STRANZINGER G.;
"An equine sequence homologous to cyclin-dependent kinase inhibitor (CDKNZA).";
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF076782; AAC97110.1;
HSSP; P42771; 1B17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "A CDKN2-like polymorphism in Xiphophorus LG V is associated with UV-B-induced melanoma formation in platyfish-swordtail hybrids."; Proc. Natl. Acad. Sci. U.S.A. 93:13042-13047(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Perissodactyla; Equidae; Equus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 235; DB 13; Length 12.
Pred. No. 9.59e-29;
13; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REVISIONS.
KAZIANIS S., NAIRN R.S.;
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, 169273: AAB09560.3; -.
HSSP; P42771; 1B17.
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1-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
CYCLIN-DEPENDENT KINASE 2A INHIBITOR (FRAGMENT).
                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BFB0B9C5 CRC32;
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                                                                                                                                                          124 AA.
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                                                                                                                                                                                                              Created)
                                                                                                                                                          PRT;
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                                                                                                                                                                                                      01-FEB-1997 (TrEMBLrel. 02, 01-MAY-1999 (TrEMBLrel. 10, 01-NOV-1999 (TrEMBLrel. 12, CDNK2X PROTEIN.
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6162 MW;
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                        Match 26.3%;
Local Similarity 51.9%;
Les 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 RLPLDLAQERGHODIVRYL 79
  CLPIDLARQNGHTDVVAVL
                                                                                                                                                          PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NON_TER
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SEQUENCE
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P70067
P70067;
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097886
097886;
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103
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Atherinomorpha;
Cyprinodontiformes; Cyprinodontoidei; Poeciliidae; Xiphophorus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                        1 MAMGNVHVAALLLNYGADSNCEDPTTFSRPVHDAAREGFLDTLVVLHGSGARLDVRDAWG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-RIO SARABIA;
STRAIN-RIO SARABIA;
STRAINS S., MORIZOT D.C., DELLA COLETTA L., JOHNSTON D.A.,
WOOLCOCK B., VIELKIND J.R., NAIRN R.S.;
"Comparative Structure and Characterization of a CDKN2 Gene in
Xiphophorus Fish Melanoma Model.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 13; Length 124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 453; DB 11; Length 86;
Pred. No. 1.42e-78;
16; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 238; DB 13; Length 12
Pred. No. 2.15e-29;
13; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-CS7BL/6J;
MALUWBRES M., PELLICER A.;
Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF013460; AAB94534.1;
HSSP; P42771; IBI7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                         01-JUN-1998 (TremBirel. 06, Last sequence update)
01-NOV-1999 (TremBirel. 12, Last annotation update)
CYCLIN-DEPENDENT KINASE INHIBITOR PISINK4B (FRAGMENT).
CDRNZB.
Created)
Last sequence update)
Last annotation update)
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SEQUENCE 124 AA; 13049 MW; DA386E94 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86 AA; 9237 MW; FEC97F63 CRC32;
                                                                                                                                                                                                                                       86 AA
                                                                                                                                                                                                                                                                                           Created)
                                                                                                                                                                                                                                       PRT;
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RLPLDLAQERGHQDIVRYLRSAG 83
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| RLPLDLAQERGHQDIVRYLRSA 82
                                                                             RLPVDLAEEQGHRDIARYLHAA 83
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06,
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01-NOV-1999 (TrEMBLEAL 12,
01-NOV-1999 (TrEMBLEAL 12,
PH3CDENUZX.
CDENUZX.
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Local Similarity 71.1%;
nes 59; Conservative
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Local Similarity 51.9%;
hes 41; Conservative
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054846
054846;
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Q9W6I8
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61

Matches

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Length 58;

Score 214; DB 6;

24.0%;

Query Match

Matches

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Created)

1194 AA

PRT;

US-09-016-869A-6.rspt

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Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                         WARAMATSO Y., MAYNARD T.M., JONES S.U., WESTON J.A.;
"NDMB localizes in the basal cortex of mitotic avian neuroepithelial
cells and modulates neuronal differentiation by binding to NOTCH-1.";
Neuron 23:71-81(1999).
EMBL; AF159231; AAD42893.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              681 VNNVEAAVVLLKNGANKDMQNNKE-ETPLFLAAREGSYETAKVLLDHFANRDITDHMDRL 739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : || | : || : || : || || || 3 MGNVHVAALLLINYGADSNCEDPTTFSRPVHDAAREGFLDTLVVLHGSGARLDVRDAMGRL 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . Match 17.5%; Score 156; DB 13; Length 1194; Local Similarity 42.9%; Pred. No. 2.01e-12; es 33; Conservative 12; Mismatches 31; Indels 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1194 AA; 130641 MW; ABEFC206 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ULT 15
093617
093617
093617
010100-1998 (TrEMBLrel. 08, C2)
01-NOV-1999 (TrEMBLrel. 08, L6)
01-NOV-1999 (TrEMBLrel. 12, L6)
                                                                    ULT 14
09W737;
09W737;
01-NOV-1999 (TEMBLE1. 12, C1
01-NOV-1999 (TEMBLE1. 12, L2
01-NOV-1999 (TEMBLE1. 12, L2
NOTCH-1 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         740 PRDIAQERMHHDIVRLL 756
  62 LPLDLAQERGHQDIVRYL 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63 PLDLAQERGHQDIVRYL 79
                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                 TISSUE-BRAIN;
MEDLINE; 99328644.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NOTCH HOMOLOGUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              178 GHEQVTRLLLKFGADVNVSGEVG-DRPLHLASAKGFLNIAKLLMEEGSKADVNAQDNEDH 236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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m
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01-NOY-1999 (TrEMBLrel. 12, Last sequence update)
01-NOY-1999 (TrEMBLrel. 12, Last annotation update)
HYPOTHETICAL 92.9 KD PROTEIN.
HYPOTHETICAL HOMO Sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mus musculus (Mouse).
Eukaryota: Metazoo; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

TISSUE-HEART;
WEI Y.J., DING J.F., XIONG H., ZHOU Y., HUI R.T., LIEW C.C.;
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, AFL16826; AAD29632.1; -.
Hypothetical protein.
SEQUENCE 835 AA; 92850 MW; DD5593A0 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 251;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
18.3%; Score 163; DB 4; Length 835;
Best Local Similarity 38.5%; Pred. No. 8.57e-14;
Matches 30; Conservative 19; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          O61905 PRELIMINARY; PRT; 251 AA.
061905 O100-1996 (TEMBLIEL. 01, Created)
01-NOV-1996 (TEMBLIEL. 01, Last sequence update)
01-NOV-1999 (TEMBLIEL. 12, Last annotation update)
NOTCH PROTEIN HOMOLOG 1 (MRNA FROM MI14 GENE) (FRAGMENT).
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                         Indels
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MESSERLE M., FOLLO M., NEHLS M., EGGERT H., BOEHM T.;
Submitted (NOV-1994) to the EMBL/GenBank/DDBJ databases.
EMBL, X82621; AAG57909.1; -.
HSSP, Q00421; LAMC.
MGD; MGI:97363; Notchl.
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Pred. No. 3.33e-13;
13; Mismatches 28;
Best Local Similarity 75.0%; Pred. No. 2.98e-24; Matches 30; Conservative 4; Mismatches 6;
                                                                    58
                                                                                                  251 AA; 27087 MW; D5FBAB3C CRC32;
                                                                      19 MMMGSVHVAELLLIHGADPNRADPDTLTRPVHDAAREGFL
                                                                                                                                                                                                                 835 AA
                                                                                                                                                                                                                 PRT;
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Best Local Similarity 43.6%;
Matches 34; Conservative
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62 LPLDLAQERGHQDIVRYL 79
                                                                                                                                                                                                                   PRELIMINARY;
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NON_TER
SEQUENCE
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735 AA

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Bukaryota, Metazoa, Chondata, Cranlata; Vertebrata, Actinopterygil;
Neopterygil; Teleostel; Euteleostel; Ostariophysi; Cypriniformes;
Cyprinoidea; Cyprinidae; Rasborinae; Danio.
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Pred. No. 7.66e-12;
14; Mismatches 29; Indels
                                                                                                                                                                                                                                         SECUENCE FROM N.A.

KIM C., YEO S., WURAOKA O., PARK H., HUH T., MIKI N.;
"Zebrafish Notch homologue 2.";
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                               EMBL; U57974; AAC17214.1; ...
HSSP; P25663; 1NFI.
HSSP; PE00023; ans. 6.
SEQUENCE 735 AA; 78567 MW; EAC8E7CF CRC32;
Created)
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Best Local Similarity 41.0%;
Matches 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            308 LPRDTAQERMHHDIVRLL 325
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Search completed: Thu Jul 20 08:43:12 2000

Job time : 20 secs.

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AR037494 Sequence 1 from pat
AR062774 Sequence 1 from pat
11148 Sequence 1 from paten
S78535 tumor suppressor gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          aGInGluargGlyHisGlnaspIleValargTyrLeuargSeralaGlyC 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MetMetMetGlyAsnValHisValAlaAlaLeuLeuLeuAsnTyrGlyAl 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17 aAspSerAsnCysGluAspProThrThrPheSerArgProValHisAspA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34 laAlaArgGluGlyPheLeuAspThrLeuValValLeuHisGlySerGly
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Gaps: 0
Percent Identity: 100.000
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                                                                                                                                                                                Unknown.
Unclassified.
1 (bases I to 507)
Stono.S., Jiang, P. and Kamb, A.
Mouse MTSI gene
Patent: US 5843756-A 44 01-DEC-1998;
 1.3e-23
1.3e-23
1.3e-23
1.9e-23
                                                                                       seq_documentation_block:
Locus
Locus
AR062814 507 bp DNA
DEFINITION Sequence 44 from patent US 5843756.
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157 c 165 g
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                                                                                                                                          AR062814.1 GI:5990505
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Ratio: 5.264
Percent Similarity: 100.000
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US-09-016-869A-6 x AR062814
                                                                  seq_name: gb_pat:AR062814
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LOCUS 189920
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                                                                                                                                                                    Unknown.
gb_pat:AR037494
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TITLE
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 AUTHORS
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 713)
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                                                                                                                           the mammalian cell cycle
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Mus musculus p19 ARF protein mRNA, complete cds.
L76092.
L76092.1 GI:1162946
p19 protein.
Mus musculus (clone: MARF) cDNA to mRNA.
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Ratio: 5.264 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
                                                          Unchanged Unclassified.

Unclassified.

1 (bases 1 to 713)

5 Sherr.C.J. and Quelle, D.E.

ARF-p19, a novel regulator of the mammar.

AL Patent: US 5723313-A 1 03-MAR-1998;

Location/Qualifiers
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Quelle, D.E., Zindy, F., Ashmun, R.A. and Sherr, C.J.
Alternative reading frames of the INK4a tumor suppressor gene encode two unrelated proteins capable of inducing cell cycle arrest Cell 83 (6), 993-1000 (1995)
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195 c
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Richer, K.H., Malker, C., Beach, D., Sherr, C.J. and Serrano, M. Cloning and characterization of murine pi6INK4a and pi5INK4b genes obcogene 11 (4), 635-645 (1995)
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L76150
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CDK4 inhibitor; CDK6 inhibitor.
Mus musculus CDNA to mRNA.
EURATUAL.
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                                                                                                                                                              117 uArgGlyGlnSerGlnGluGlnSer 125
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BASE COUNT
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Location/Qualifiers
S80650 713 bp mRNA ROD 02-APR-199 p16INK4a-CDK4 and CDK6 cyclin D-dependent kinases inhibitor (alternatively spliced, exon 1 beta and exon 2) [mice, MEL erythroleukemia cells, mRNA Partial, 713 nt]. S80650 S80650 GI:1245977
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 436 CCAAGAGCGGGACATCAAGACATCGTGCGATATTTGCGTTCCGCTGGGT 485
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DEFINITION
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VERSION
KEYWORDS
SOURCE
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ORIGIN
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Butheria; Rodenita; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 849)
2hang, S., Ramsay, E.S. and Mock, B.A.
2ckn2a, Remsay, E.S. and Mock, B.A.
and pl9(Ref.), is a candidate for the plasmacytoma susceptibility locus, pctrl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (23-JAN-1998) NCI/LG, NIH, 37 Convent Dr., Bethesda, MD 20892, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BALB/chapt cyclin dependent kinase inhibitor NNA, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 95 (5), 2429-2434 (1998) 98151529
                                                                                                                                                                                                                 1 MetMetMetGlyAsnValHisValAlaAlaLeuLeuLeuAsnTyrGlyAl 17
                                                                                                                                                                                                                                                                       17 aAspSerAsnCysGluAspProThrThrPheSerArgProValHisAspA 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67 aGlnGluArgGlyHisGlnAspIleValArgTyrLeuArgSerAlaGlyC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  101 GlnThrAspGlyHisSerPheSerSerThrProArgAlaLeuGluLe
                                                                                                                                                                                                                                                                                                                                                                                                                          51 AlaArgLeuAspValArgAspAlaTrpGlyArgLeuProLeuAspLeuAl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84 ysSerLeuCysSerAlaGlyTrpSerLeuCysThrAlaGlyAsnValAla
                   Length: 125
Gaps: 0
Percent Identity: 100.000
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Zhang,S., Ramsay,E.S. and Mock,B.A.
Direct Submission
                                                                                                                                                         to: 849
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Mus musculus strain BALB/CAnPt cy
p16INK4a (Cdkn2a) mRNA, complete
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1. .849
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /strain="BALB/cAnPt"
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                                                                                                                                                         Align seg 1/1 to: AF044336
                 Quality: 658.00
Ratio: 5.264
Percent Similarity: 100.000
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US-09-016-869A-6 x AF044336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_name: gb_ro:AF044335
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     alignment_scores
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KEYWORDS
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Abangy. N. Ramsay. E.S. and Mock, B.A.
Direct Submission
Submitted (23-JAN-1998) NCI/LG, NIH, 37 Convent Dr., Bethesda, MD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodenita; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 849)
Zhang, S., Ramsay, E.S. and Mock, B.A. Cdkn2a, the cyclin-dependent kinase inhibitor encoding p16(INK4a) and p19(ARF), is a candidate for the plasmacytoma susceptibility
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AF044336 849 bp mRNA ROD 01-APR-1998 Mus musculus strain DBA/2N cyclin dependent kinase inhibitor AF044336
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Proc. Natl. Acad. Sci. U.S.A. 95 (5), 2429-2434 (1998)
98131529
                                                                                                                                                                                           457
                                                                                                                                                                                                                               84 ysSerLeuCysSerAlaGlyTrpSerLeuCysThrAlaGlyAsnValAla 100
                                                                                                                 358 GCTCGGCTGGATGTGCGCGATGCCTGGGGTCGCCTGCCGCTCGACTTGGC 407
                                                                           67
                                                                                                                                                         84
aGlnGluArgGlyHisGlnAspIleValArgTyrLeuArgSerAlaGlyC
                                                                                                                                                                                                                                                                                                                               508 CAGACCGACGGCATAGCTTCAGCTCAAGCACGCCCAGGGCCCTGGAACT
                                                                         51 AlaArgLeuAspValArgAspAlaTrpGlyArgLeuProLeuAspLeuAl
                                                                                                                                                                                           408 CCAAGAGCGGGACATCAAGACATCGTGCGATATTTGCGTTCCGCTGGGT
                                                                                                                                                                                                                                                                       458 GCTCTTTGTGTTCCGCTGGGTGGTCTTTGTGTACCGCTGGGAACGTCGCC
                                                                                                                                                                                                                                                                                                             GlnThrAspGlyHisSerPheSerSerSerThrProArgAlaLeuGluLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /map="1.8 cM distal to Ifna"
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    .849
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/tissue_type="spleen"
/chromosome="4"
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JS AF044336
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84

29

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(MSB 594), New York University New York, NY 10016, USA

BASE CC ORIGIN

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                                                                                Mangues, R., Serrano, M., Pellicer, A. and Fernandez-Piqueras, J. Inactivation of the cyclin-dependent kinase inhibitor pi5INK4b deletion and de novo methylation with independence of pi6INK4a alterations in murine primary T-cell lymphomas
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 482)
Malumbres, M., Perez de Castro, I., Santos, J., Molendez, B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84 ysSerLeuCysSerAlaClyTrpSerLeuCysThrAlaClyAsnValAla 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  107 ATGATGATGGGCAACGTTCACGTAGCAGCTCTTCTGCTCAACTACGGTGC 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34 laAlaArgGluGlyPheLeuAspThrLeuValValLeuHisGlySerGly 50
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                                                                                                                                                                                    2 (bases 1 to 482)
Malumbres, M. and Pellicer, A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product-"p16INK4a'
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Ratio: 5.327
Percent Similarity: 100.000
musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus cyclin-dependent kinase inhibitor (p16INK4a) gene, decom 2 and partial cds.
                                                                                      82. .588
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          261 AGATTCGAACTGCGAGGACCCCACTACTTCTCCCGCCCGGTGCACGACG 310
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217 c
                                                     .849
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Ratio: 5.256
Percent Similarity: 100.000
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LOCUS MMINK4A02
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house mouse.
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                                                                                                                                                                                                                                                                                           188
                                                                                                                                                                                                                                                                                                                                                                    alignment_scores:
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                                                   gene
                                                                                                                                                                                                                                                                                               COUNT
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KEYWORDS
SEGMENT
SOURCE
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cyclin-dependent kinase inhibitor

34

to: 482

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DEFINITION

ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

REFERENCE AUTHORS

JOURNAL REFERENCE AUTHORS

TITLE

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MMU79633 339 bp DNA ROD 05-JAN-1999
Mus musculus cyclin-dependent kinase inhibitor protein (p16(INK4a))
U79633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Santos,J., Melendez,B., Perez de Castro,I., Malumbres,M., Serrano,M., Pellicer,A. and Fernandez-Piqueras,J. Comparative analysis of the p16(INK4a) and p15(INK4b) DNA sequences in mouse inbred strains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation-"vmmmGNVHVAALLLNYGADSNCEDPTTFSRPVHDAAREGFLDTL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 (bases I to 339)
Santos, J., Melendez, B., Perez de Castro, I., Malumbres, M.,
Santos, M., Pellider, A. and Fernandez-Piqueras, J.
Direct Submission
Submission
Submitted (09-007-1996) Biologia, Universidad Autonoma de Madrid,
Cantoblanco, Madrid, Madrid 28049, Spain
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product-"cyclin-dependent kinase inhibitor protein"
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 339)
                  84 ysSerLeuCysSerAlaGlyTrpSerLeuCysThrAlaGlyAsnValAla 100
                                                                                                                                                                                                                                                                                                                                  254 GCTCTTTGTGTTCCGCTGGTGTCTTTGTGTACCGCTGGGAACGTCGCC 303
                                                                                                                                                                                                   67 aGlnGluArgGlyHisGlnAspIleValArgTyrLeuArgSerAlaGlyC 84
                                                                                                                                                                                                                              51 AlaArgLeuAspValArgAspAlaTrpGlyArgLeuProLeuAspLeuAl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 112
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                                                                                                                                                                                                                                                                                                                                                                                                        304 CAGACCGACGGCATAGCTTCAGCTCAAGCACGCCC 339
                                                                                                                                                                                                                                                                                                                                                                            101 GlnThrAspGlyHisSerPheSerSerSerThrPro 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="p16(INK4a)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_documentation_block:
LOCUS MMU79633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name: gb_ro:MMU79633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       house mouse.
Mus musculus
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ORGANISM
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AUTHORS
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                          Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 339)
Santos,J., Melendez,B., Perez de Castro,I., Malumbres,M., Serrano,M., Pellicer,A. and Fernandez-Piqueras,J.
Comparative analysis of the p16(INK4a) and p15(INK4b) DNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="cyclin-dependent kinase inhibitor protein"
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                                                                                                                                                                MSU79634 339 bp DNA ROD 05-JAN-1999
Mus spretus cyclin-dependent kinase inhibitor protein (pl6(INK4a))
gene, exon 2 and partial cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Santos, J., Melendez, B., Perez de Castro, I., Malumbres, M., Sentos, J., Melendez, B., Perez de Castro, I., Malumbres, M., Serrano, M., Pellicer, A. and Fernandez-Piqueras, J. Direct Submission
Submitted (09-OCT-1996) Biologia, Universidad Autonoma de Madrid, Cantoblanco, Madrid, Madrid 28049, Spain
Location/Qualifiers
357 GCTCTTTGTGTTCCGCTGGGTGTTTTGTGTACCGCTGGGAACGTCGCC 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 ATGATGATGGGCAACGTTCACGTAGCAGCTCTTCTGCTCAACTACGGTGC 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17 aAspSerAsnCysGluAspProThrThrPheSerArgProValHisAspA 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MetMetGlyAsnValHisValAlaAlaLeuLeuLeuAsnTyrGlyAl 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length: 112
Gaps: 0
Percent Identity: 100.000
                                                                 101 GlnThrAspGlyHisSerPheSerSerSerThrProArg 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /map-"between C3 and C6 bands"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to: 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1. 339
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1. .339
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Unpublished
                                                                                                                                                                                                                                                                                         U79634.1 GI:4098165
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                                                                                                                                                                                                                                                                                                                                  western wild mouse.
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Ratio: 5.330
Percent Similarity: 100.000
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                                                                                                                                                                              seq_documentation_block:
LOCUS MSU79634
                                                                                                                                  seq_name: gb_ro:MSU79634
                                                                                                                                                                                                                                                                                                                                                          Mus spretus
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source

FEATURES

JOURNAL

TITLE

gene

exon

CDS

alignment_scores:

BASE COUNT

alignment_block

Align seg 1/1

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138 t 188 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-167

181167

ON Rattus norvegicus pl6 protein (Pl6INK4a) mRNA, complete cds.

N 181167

181167.1 GI:5732019

protein pl6.

ON Rattus norvegicus

Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

E 1 (bases 1 to 707)

Swafford.D.S., Middleton, S.K., Palmisano, W.A., Nikula, K.J., Tesfaigzi, J., Baylin, S.B., Herman, J.G. and Belinsky, S.A.
                                                                                                                                                                                                                                                              67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MetMetMetGlyAsnValHisValAlaAlaLeuLeuLeuAsnTyrGlyAl 17
                                                                                                                       51 AlaArgLeuAspValArgAspAlaTrpGlyArgLeuProLeuAspLeuAl
                                                   34 laAlaArgGluGlyPheLeuAspThrLeuValValLeuHisGlySerGly
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Gaps: 2
Percent Identity: 73.600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mol. Cell. Biol. 17 (3), 1366-1374 (1997)
97184461
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                                                                                                                                                                                                                                                                                                                                                                     301 CAGACCGACGGGCATAGCATCAGCTCAAGCACGCCC 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
1. .707
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4.351
83.200
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US-09-016-869A-6 x L81167
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Locus L81167
                                                                                                                                                                                                                                                                                                                                                                                                           seq_name: gb_ro:L81167
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Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                157
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VERSION
KEYWORDS
SOURCE
ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORIGIN
                                                                                                                                                                                                                                                                                                                  Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 336)
Santos,J., Melendez,B., Perez de Castro,I., Malumbres,M.,
Serrano,M., Pellicer,A. and Fernandez-Piqueras,J.
Comparative analysis of the p16(INK4a) and p15(INK4b) DNA sequences
in mouse inbred strains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="pl6(lNK4a)"
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                                                                                                                                                                                                             protein (pl6(INK4a))
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished

2 (bases 1 to 336).

2 santos,J., Malumbres,M.,
Santos,J., Malendez,B., Perez de Castro,I., Malumbres,M.,
Serrano,M., Pellicer,A. and Fernandez-Piqueras,J.
Direct Submission
Submitted (09-OCT-1996) Biologia, Universidad Autonoma de Madrid,
Cantoblanco, Madrid, Madrid 28049, Spain
Location/Qualifiers
                                                                                                                                                                                              05-JAN-1999
 84 ysSerLeuCysSerAlaGlyTrpSerLeuCysThrAlaGlyAsnValAla 100
                254 GGTCTTTGTGTTCCGCTGGGTGGTCTTTGTGTACCGCTGGGAACGTCGCC 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17 aAspSerAsnCysGluAspProThrThrPheSerArgProValH1sAspA 34
                                                                                                                                                                        seq_documentation_block:
LOCUS MMU79635 336 bp DNA
DEFINITION Mus musculus cyclin-dependent kinase inhibitor
gene, exon 2 and partial cds.
ACCESSION U79635.1 GI:4098155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps: 1
Percent Identity: 97.321
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                                                                Length:
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/gene="p16(INK4a)"
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99.107
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AUTHORS
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176 ATGATGATGGCCAACGTCAAAGTGGCAGCTCTCCTGCTCTCCTATGGTGC 225
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17 alenSerbenCueG]lenDr.OmhrmhrDheCorlardDr.OVa]Hielenh 34	

²²⁶ AGATICGAACIGCGAGGACCCCACCACCTCTCCCGACCGGIGCACGACG 275

Multiple tumour suppressor 2 Human multiple tumour suppre Human multiple tumour suppre Human MTS2 CDNA. DNA specifi

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Claim 1; Fig 18; 80pp; English.
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01-DEC-1998.
28-JUL-1995; 058735.
28-JUL-1995; US-508735.
07-JUN-1995; US-487033.
(MYRI-) MYRIAD GENETICS INC.
Jiang P, Kamb A, Stone S;
WHI; 99-044885/04.
                                                                                    seq_documentation_block:
ID V70623 standard; cDNA; 507 BP.
AC V70623;
329.00
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                                                                                                                            03-FEB-1999 (first entry)
                                                                seg_name: N_Geneseg_36:V70623
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Ratio: 5.264
Percent Similarity: 100.000
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N_Geneseq_36:T00745
N_Geneseq_36:Q99165
N_Geneseq_36:T69781
N_Geneseq_36:V11250
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                                                                                                     Documentation

Mouse multiple tumour suppresson

Murine ARF pl9 cDNA, Nucleic ac

Cell-cycle regulatory protein p

Mouse pi6 cDNA fragment. DNA sp

Nucleotide sequence of nucleic

CDNA encoding a murine multiple

Multiple tumour suppressor i

Human MrSI genomic DNA includi

Coding sequence 2 of the multiple

Human multiple tumour suppress

Multiple tumour suppress

Multiple tumour suppress
                                                                                               About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
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338 50 655 49

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Database length: 125096042
Search time (sec): 109.050000
                        Date: Jul 21, 2000 9:30 AM
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Query: US-09-016-869A-6
Query length: 125
Database: N_Geneseq_36:*
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N.Geneseq. 36: 702965

N.Geneseq. 36: 7020965

N.Geneseq. 36: 70004

N.Geneseq. 36: 710140

N.Geneseq. 36: 710140

N.Geneseq. 36: 710140

N.Geneseq. 36: 710141

N.Geneseq. 36: 710144

N.Geneseq. 36: 710148

N.Geneseq. 36: 710138

N.Geneseq. 36: 710138
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N_Geneseq_36:T15155
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N_Geneseq_36:T74053
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N_Geneseq_36:X26231
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                                                                                                                                                                                                                                                                                                                                                                                    score_list:
Sequence
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Mouse multiple tumour suppressor gene segment - useful for primer
Mouse multiple tumour suppressor 1 gene (MTS1) coding sequence. Muxine; multiple tumour suppressor 1 gene; MTS1; cancer; ss. Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence encodes mouse multiple tumour suppressor (MTS1) gene. The MTS1 gene can be used to design primers to detect abnormalities i.e. polymorphisms which may predispose towards malignancies such as melanoma, leukaemia, astrocytoma, lymphoma, q110nma, as well as tumours of e.g. the breast, thyroid, pancreas, uterus and kidneys. 165 G; 99 T; sequence 507 BP; 86 A; 157 C; 165 G; 99 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                130 ATGATGATGGCCAACGTTCACGTAGCAGCTCTTCTGCTCAACTACGGTGC 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84
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                                                                                                                            /*tag= a
126. .127
/*tag= b
/note= "splice site"
467. .468
                                                                                                                                                                                                                                                               /note= "splice site"
                                                                                    Location/Qualiflers
1..507
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PPD 03-ARPH1997.

PPD 21-SEP-1995; US-534975.

PR 27-SEP-1995; US-534975.

PR (57UD-) ST UUDE CHILDREN'S RES HOSPITAL.

DE GALDL DE, Sherr CJ;

Quelle DE, Sherr CJ;

WPL; 97-212919/19.

DR WPL; 97-212919/19.

PP PEDB; W16311-22.

PP Torug screening

PP Transcripts (see also T62486) homologous to human INK4A beta are conversible and cell DNA 11brary. Sequences of exon 1-beta are spliced to exon 2 to create an open reading frame that encodes a cythrologus converspressed. Unrelated sequences from a mouse crythrologusamia cell DNA 11brary. Sequences of exon 1-beta are spliced to exon 2 to create an open reading frame that encodes a novel protein, ARF-P19 (W16321), which induces cell cycle arrest when overexpressed. Unrelated sequences from exon 1-alpha (not spliced to the same exon 2 acceptor site to open another chown) are spliced to the same exon 2 acceptor site to open another reading frame that encodes InK41a-p16 (C-terminal fragment given in W16322), an inhibitor of the cyclin D-dependent Kinases CDK4 and CDK6. Economical reutilisation of protein coding sequences in this manner is without precedent in mammalian genomes and the unitary concerned the proteins in cell cycle control. ARF-P19 nucleic acids can be used as probes or primers, or in gene therapy protocols to induce cell arrest in eukaryotes or (antisense) to inhibit ARF-P19 activity, and to create transgenic animals useful as models for cancer. Human ARF-P19 CDA 223 G; 162 T;
                                                                                                                                                                                                                                                                                                                                                                      16-AUG-1997 (first entry)
Murine ARF-p19 cDNA.
Murine ARF-p19 alternative reading frame; cell cycle; cancer; diagnosis;
gene therapy; INK4a-p16; cyclin D-dependent kinase; CDK4; CDK6;
inhibitor; ss.
84 ysSerLeuCysSerAlaGlyTrpSerLeuCysThrAlaGlyAsnValAla 100
                      101 GlnThrAspGlyHisSerPheSerSerThrProArgAlaLeuGluLe 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product INK4a.p16 C.terminal fragment
1, .232
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233..702
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/note= "Exon 2"
complement (56. .75)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers 43. .552
                                                                                                                                                                         117 uArgGlyGlnSerGlnGluGlnSer 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag= a
/product= ARF-p19
                                                                                                                                                                                                  seq_documentation_block:
ID T62485 standard; cDNA; 713 BP
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/note= "5' |
602. .624
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/note= "3'
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01-MAR-1996 (first entry)
Cell-cycle regulatory protein p13.5 cDNA.
Cell-cycle regulatory protein p13.5; cyclin-dependent kinase inhibitor;
Cell-cycle regulatory protein p13.5; cyclin-dependent kinase inhibitor;
CCR; gene therapy; transgenic animal; cancer; cell proliferation;
ss; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New cell cycle regulating proteins bind to cyclin dependent kinase and related nucleic acids, antibodies etc., used in diagnosis and therapy of abnormal cell proliferation, degeneration etc. Example 4; Page 80; 109pp; English.
                                                                                                                                                                                                                                                                285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 436 CCAAGAGCGGGACATCAAGACATCGTGCGATATTTGCGTTCCGCTGGGT 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84 ysSerLeuCysSerAlaGlyTrpSerLeuCysThrAlaGlyAsnValAla 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        535
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                                                                                                                                                                                                                                                                                                         17 aAspSerAsnCysGluAspProThrThrPheSerArgProValHisAspA 34
                                                                                                                                                                                                                                              1 MetMetMetGlyAsnValHisValAlaAlaLeuLeuLeuAsnTyrGlyAl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      486 GCTCTTTGTGTTCCGCTGGGTGGTCTTTGTGTATACCGCTGGGAACGTCGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67 aGlnGluArgGlyHisGlnAspIleValArgTyrLeuArgSerAlaGlyC
                                                           Percent Identity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
213. .590
/*tag= a
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14-APR-1994; US-227371.
25-MAY-1994; US-248812.
14-SFP-1994; US-346511.
29-NOY-1994; US-346147.
(COLD-) COLD SPRING HARBOR LAB.
                                                                                                                                                                           from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T02965 standard; cDNA; 853 BP. T02965;
                Quality: 658.00
Ratio: 5.264
Percent Similarity: 100.000
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                                                                                                                                                                         Align seg 1/1 to: T62485
                                                                                                       alignment_block:
US-09-016-869A-6 x T62485
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alignment_scores
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MYRI-) MYRIAD GENETICS INC.

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Mouse p16 cDNA fragment.
MTS1; WTS2; WTS1E1-beta; multiple tumour suppressor; diagnosis; cancer;
germ-line mutation; familial melanoma locus; MLM; predisposition; ds.
cDNA (T0295) coding for the mouse cell-cycle regulatory (CCR) protein p13.5 (R85120) was isolated from an embryonal stem cellibrary using a probe based on human CCR p16 cDNA (T02962). The isolated cDNA can be used: to detect mutations in CCR genes that lead to cell proliferation, to bread transgenic animals to study cellular disorders involving CCR allele mutation/misexpression; and to correct CCR-deficient cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84 ysSerLeuCysSerAlaGlyTrpSerLeuCysThrAlaGlyAsnValAla 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                       312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84
                                                                                                                                                                                                                                                                                                                                      1 MetMetMetGlyAsnValHisValAlaAlaLeuLeuLeuAsnTyrGlyAl 17
                                                                                                                                                                                                                                                                                                                                                                                                     17 aAspSerAsnCysGluAspProThrThrPheSerArgProValHisAspA 34
                                                                                                                              180
                                                                                                                                                                                                                                                                                                                                                                                                                        34 laAlaArgGluGlyPheLeuAspThrLeuValValLeuHisGlySerGly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                463 GCTCTTTGTGTTCCGCTGGGTGTCTTTGTGTACCGCTGGGAACGTCGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          101 GlnThrAspGlyHisSerPheSerSerSerThrProArgAlaLeuGluLe
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Ratio: 5.264 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
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                                                                                                                              207
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                                                                                                                              192 A;
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    V11259 standard; cDNA; 395
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_name: N_Geneseq_36:V11259
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US-214582.
US-215086.
US-215087.
US-215087.
US-251938.
WO-U03316.
                                                                                                                                                                                                                                                                                                       Align seg 1/1 to: T02965
                                                                                                                                                                                                                                                       alignment_block:
US-09-016-869A-6 x T02965
                                                                                                           (gene therapy).
Sequence 853 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-APR-1998.
07-JUN-1995; 4
07-JUN-1995; 0
18-MAR-1994; U
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14-APR-1994; 1
01-JUN-1994; 1
17-MAR-1995; v
                                                                                                                                                                            alignment_scores:
                                                                                                                               Sequence
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DNA specific for Multiple Tumour Suppressor IEI-beta gene - are useful for the diagnosis of cancers related to MTSIEI-beta mutation(s) and their treatment to mutation(s) and their treatment bisclosure; Figure 14: 72pp; English.

This is a mouse pl6 cDNA sequence used in the characterisation of the human multiple tumour suppression proteins, MTSI, MST2 and MTSIEI-beta. The MTS gene locus is also referred to as the familial melanoma (MLM) gene locus, located on human chromosome 9p21. Germ line mutations in MTS genes can be used in the diagnosis of predisposition to cancers, e.g. melanoma, leukaemia, astrocytoma, gliboblastoma, lymphoma, glioma, Hodgkin's lymphoma, CLL, and cancers of the pencreas, breast, thyroid, ovary, uterus, testis, kidney, stomach and rectum.

Sequence 395 BP; 73 A; 109 C; 128 G; 85 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-DEC-1998 (first entry)
Nociectide sequence of nucleic acid 6.
Multiple tumour suppressor; MTSLEIS; human; cancer; hybridisation; somatic mutation; gene therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    240 CAGCGCGCGAAGGCTTCCTGGACACGCTGGTGGTGCTGCACGGGTCAGGG 289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MetMetMetGlyAsnValHisValAlaAlaLeuLeuLeuAsnTyrGlyAl
                                                                                                                                                                                                                                                                                                                                         Gaps:
Percent Identity: 98.
                                                                                                                                                                                                                                                                                                                                                                                                                                             to: 395
                                                                                                                                                                                                                                                                                                                                                                                                                                             from: 1
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01-SEP-1998.
07-JUN-1995; US-480810.
07-JUN-1995; US-214582.
18-MAR-1994; US-214582.
18-MAR-1994; US-215086.
18-MAR-1994; US-215086.
14-APR-1994; US-227369.
01-JUN-1994; US-227369.
17-MAR-1995; WO-U0316.
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                                                                                                                                                                                                                                                                                                                     Quality: 445.00
Ratio: 5.235
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to: V11259
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US-09-016-869A-6 x V11259
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               Kamb A;
WPI; 98-250421/22
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GENETICS INC

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18-MAR-1994;
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    Disclosure: Column 83-84; 73pp; English.

Disclosure: Column 83-84; 73pp; English.

This is the nucleotide sequence of a nucleic acid used in the method of the invention involving the used of the multiple tumour compares of the nucleotide sequence and treat human cancers. The MTS gene is useful in the diagnosis and prognosis of human cancer, e.g. cran setul in the diagnosis and prognosis of patient samples.

The mutated sequences are those that are present in somatic mutations of the gene in cancers. The vectors can be used for gene therapy of the gene in cancers. The vectors can be used for gene therapy of strategies to replace function of mutated protein in patients. These can also be used to construct protein mimetics, also for therapeutic strategies. In addition the expression constructs can also be used to construct production of MTS. Recombinant MTS can be used to screen for drugs to be used for cancer therapy, and the protein construct sequence 395 BP; 73 A; 109 C; 128 G; 85 T;
Kamb A;
WPI; 98-494842/42.
Nucleic acids based on multiple tumour suppressor, MTS, sequences -
useful as hybridisation probes, primers and recombinant production
of MTS in the diagnosis and treatment of cancers related to MTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-FEB-1999 (first entry)
CDNA encoding a murine multiple tumour suppressor 1E1-beta p
Murine; multiple tumour suppressor 1 gene; MTS1; cancer; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              240 CAGCGCGCGAAGGCTTCCTGGACACGCTGGTGGTGCTGCACGGGTCAGGG 289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34 laAlaArgGluGlyPheLeuAspThrLeuValValLeuHisGlySerGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            aAspSerAsnCysGluAspProThrThrPheSerArgProValHisAspA
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                                                                                                                                                                                                                                                                                                                                                                                                    Percent Identity: 98.824
                                                                                                                                                                                                                                                                                                                                                                       Length:
                                                                                                                                                                                                                                                                                                                                                                                         Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to: V53840 from: 1 to: 395
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   V70604 standard; cDNA; 395 BP
                                                                                                                                                                                                                                                                                                                                                                      Quality: 445.00
Ratio: 5.235
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                         alignment_scores:
Quality:
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Design

Example 8; Fig 14; 80pp; English.

The present sequence encodes murine multiple tumour suppressor IEI-beta

The present sequence encodes murine multiple tumour suppressor IEI-beta

(MTSIEI-beta) protein. Primers designed from the gene can be used to
design primers to defect abnormalities i.e. polymorphisms which may
predispose towards malignancies such as melanoma, leukaemia,
astrocytoma, lymphoma, glioma, as well as tumours of e.g. the breast,
thyroid, pancreas, uterus and kidneys.

Sequence 395 BP; 73 A; 109 C; 128 G; 85 T;
                           Mouse multiple tumour suppressor gene segment – useful for primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-MAY-1996 (first entry)
Multiple tumour suppressor 1 (MTS1) gene exon 2 contg. fragment.
Multiple tumour suppressor; MTS1; cancer; diagnosis; assay;
predisposition; melanoma; leukaemia; lymphoma; prognosis;
pancreas; breast; thyrold; exon 2; ds.
Homo saplens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        190 AGAITCGAACIGCGAGGACCCCACIACCIICICCCGCCCGGIGCACGACG 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 240 CAGCGCGCAAAGCTTCCTGCACCACGCTGGTGCTGCTGCACGGGTCAGGG 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                290 GCTCGGCTGGGATGTCCGCGATGCCTGGGGTCGCCTCCCCGCTCGACTTCGC 339
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                                                                                                                                                                                                                                                                                                                                        Length: 85
Gaps: 0
Percent Identity: 98.824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               from: 1 to: 395
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/label= intron
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/label= exon 2
499. .1187
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Ratio: 5.235
Percent Similarity: 100.000
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US-214582.
US-215087.
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US-09-016-869A-6 x V70604
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WPI; 99-044585/04
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17-MAR-1995; U
18-MAR-1994; U
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Defecting polymorphism associated with cancer pre:disposition - also DNA, vectors and host cells e.g. for gene or protein replacement therapy and drug screening claim 13; Pages 94-95; Id8pp; English.

An individual can be diagnosed as having a predisposition to cancer by detecting an alteration in the wild type multiple tumour suppressor (MTS) gene, using gene probes which hybridise to exn 1 (T00737) or exon 2 (T00739) of the MTS1 gene. The above assay can also be used in the diagnosis and prognosis of melanoma, lymphoma, leukaemia and pancreas, Dreast and thyroid cancers, etc. .

Sequence 1187 BP; 243 A; 354 C; 331 G; 255 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                295 CTGCCCGGGAGGGCTTCCTGGACACGCTGGTGGTGCTGCACCGGGCCGGG 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     444
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34 laAlaArgGluGlyPheLeuAspThrLeuValValLeuHisGlySerGly
                                                                                                                                                                                                                                                                                 Length: 139
Gaps: 2
Percent Identity: 52.518
                                                                  Skolnick MH;
                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to: T00739 from: 1 to: 1187
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Human MTS1 genomic DNA including exon
         14-APR-1994; US-227369.
01-JUN-1994; US-251938.
(WYRI.) WYRIAD GENETICS INC.
(UTAH ) UNIV UTAH RES FOUND.
Cannon-Albright LA, Kamb A, S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_documentation_block:
ID V11240 standard; DNA; 1187 BP.
AC V11240;
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3.319
73.381
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                                                                                                                                                                                                                                                                                   Quality:
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Percent Similarity:
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With the following the following states of the paners of the process of the familiar and their treatment of the familiar treatment of the familiar and their treatment of the familiar bisclosure; Fig 6; 72pp; English.

Disclosure; Fig 6; 72pp; English.

This sequence encodes the human multiple tumour suppression protein, MTS1, exon 2. The MTS gene locus is also referred to as the familiar melanoma (MLM) gene locus; located on human chromosome 9p21. Germ line matations in MTS genes can be used in the diagnosis of predisposition to cancers, e.g. melanoma, leukaemia, astrocytoma, gliboblastoma, lymphoma, glidoma, Hodgkin's lymphoma, Lit, and cancers of the pancreas, breast, thyroid, ovary, uterus, testis, kidney, stomach and rectum.

Sequence 1187 BP; 243 A; 354 C; 331 G; 255 T;
WTS1; multiple tumour suppressor; diagnosis; cancer; germ-line mutation;
familial melanoma locus; MLM; predisposition; ds.
                                                                                                                                                                                                      ά
                                                                                                                      /*tag= a
/product= MTS1
/note= "Partial coding region of multiple tumour
suppressor protein which is interrupted the introns 1 and 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  245 GGAGCCCAACTGCGCCGACCCCGCCACTCTCACCCGACCGTGCACGACG 294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            345 GCGCGGCTGGACGTGCGGATGCCTGGGGCCGTCTGCCCGTGGACCTGGC 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MetMetMetGlyAsnValHisValAlaAlaLeuLeuLeuAsnTyrGlyAl 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51 AlaArgLeuAspValArgAspAlaTrpGlyArgLeuProLeuAspLeuAl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17 aAspSerAsnCysGluAspProThrThrPheSerArgProValHisAspA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34 laAlaArgGluGlyPheLeuAspThrLeuValValLeuHisGlySerGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Identity: 52.518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to: 1187
                                                                     Location/Qualifiers
1. .1187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to: V11240 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-MAR-1994; US-215086.

18-MAR-1994; US-215087.

14-APR-1994; US-227369.

01-UUN-1994; US-221938.

17-MAR-1995; WO-U03316.

(MYRI-) MYRIAD GENETICS INC.
                                                                                                                                                                                                                                                                      /*tag b //number 1 192. 498 //tag c //number 2 499. 1187 //tag d //number 2 //tag d //number 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quality: 338.50
Ratio: 3.319
nilarity: 73.381
                                                                                                                                                                                                                                               1. .191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     487033.
US-487033.
US-214582.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kamb A;
WPI; 98-250421/22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US5739027-A.
14-APR-1998.
07-JUN-1995; 4
07-JUN-1995; U
18-MAR-1994; U
18-MAR-1994; U
                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_block
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                                                                                                                                                                                                                                                    intron
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alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mutation(s)
Claim 1: Fig 6A-6B: 73pp: English.
Claim 1: Fig 6A-6B: 73pp: English.
This is the nucleotide sequence of the invention. The MTS gene
This is the nucleotide sequence of the invention. The MTS gene
is useful in the diagnosis and prognosis of human cancer. e.g. by
strandard nucleic hybridisation techniques, of patient samples. The
mutated sequences are those that are present in somatic mutations
of the gene in cancers. The vectors can be used for gene therapy
strategies to replace function of mutated protein in patients. These
can also be used to construct protein mimmetics, also for therapeutic
strategies. In addition the expression constructs can also be used
for recombinant production of MTS. Recombinant MTS can be used to
screen for drugs to be used for cancer therapy, and the protein
itself may also be used to restore MTS function in a cell.
Sequence 1187 BP: 243 A; 354 C; 331 G; 255 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                         v53821;
04-DEC-1998 (first entry)
Coding sequence 2 of the multiple tumour suppressor 1.
Multiple tumour suppressor 1; MTS-1; human; cancer; hybridisation;
somatic mutation; gene therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acids based on multiple tumour suppressor, MTS, sequences useful as hybridisation probes, primers and recombinant production of MTS in the diagnosis and treatment of cancers related to MTS
                   98 ......AsnValAlaGlnTh 102
                                                                                                                                                                                   495 TCAGGTGAGGACTGATGATCTGAGAATTTGTACYCTGAGAGCTTCCAAAG 544
                                                                                                                                                                                                                                                           545 CTCAGAGCATTCATTTTCCAGCACAGAAAGTTCAGCCCGGGAGACCAGTC 594
                                                                                                            445 GGGCACCAGAGGCAGTAACCATGCCCGCATAGATGCCGCGGAAGGTCCC 494
                                                                      84 ysSerLeuCysSerAlaGlyTrpSerLeuCysThrAlaGly......97
67 aGlnGluArgGlyHisGlnAspIleValArgTyrLeuArgSerAlaGlyC 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
1. .191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag= c
/note= "intron 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag= a
/note= "intron 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          192. .498
/*tag= b
/note= "exon 1"
499. .1187
                                                                                                                                                                                                                                                                                                                                                                                                        seq_documentation_block:
ID V53821 standard; cDNA; 1187 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-SEP-1998.

07-JUN-1995; 480810.

07-JUN-1995; US-480810.

18-MAR-1994; US-214582.

18-MAR-1994; US-215086.

14-APR-1994; US-215087.

14-APR-1994; US-251938.

17-MAR-1995; WO-U03316.
                                                                                                                                                                                                                                                                                           117 euArgGlyGlnSerGln 122
                                                                                                                                                                                                                                                                                                                    595 TCCGGTCTTGCGCTCAG 611
                                                                                                                                                                                                                                                                                                                                                                    seq_name: N_Geneseq_36:V53821
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WPI; 98-494842/42.
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01-DEC-1998.
28-UTL-1995; 058735.
28-UTL-1995; US-508735.
07-UTN-1995; US-487033.
(MYRL-) MYRIAD GENETICS INC.
Jiang P, Kamb A, Stone S;
WPI; 99-044585/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human multiple tumour suppressor 1 (MTS1) DNA fragment.
Human; multiple tumour suppressor 1 gene; MTS1; cancer; ds.
                                                                                                                                     344
                                                                                                                                                                                                                                                                                                                                                              495 TCAGGTGAGGACTGATGATCTGAGAATTTGTACYCTGAGAGCTTCCAAAG 544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 102 rAspGlyHisSerPheSerSer.....SerThrProArgAlaLeuGluL 117
                                                                                                                                                                            34
                                                                                                                                                                                                                                34 laAlaArgGluGlyPheLeuAspThrLeuValValLeuHisGlySerGly 50
                                                                                                                                                                                                                                                                                   67
                                                                                                                                                                                                                                                                                                                                     67 aGlnGluArgGlyHisGlnAspIleValArgTyrLeuArgSerAlaGlyC 84
                                                                                                                                                                                                                                                                                                                                                                                          84 ysSerLeuCysSerAlaGlyTrpSerLeuCysThrAlaGly...... 97
                                                                                                                                                                                         545 CTCAGAGCATTCATTTTCCAGCACAGAAAGTTCAGCCCGGGAGACCAGTC
                                                                                                                       1 MetMetMetGlyAsnValHisValAlaAlaLeuLeuLeuAsnTyrGlyAl
                                                                                                                                                                           17 aAspSerAsnCysGluAspProThrThrPheSerArgProValHisAspA
                Gaps: 2
Percent Identity: 52.518
                                                                                                to: 1187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             design
Example 6; Fig 6A-B; 80pp; English.
                                                                                             Align seg 1/1 to: V53821 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_documentation_block:
1D V70588 standard; DNA; 1187 BP.
AC V70585;
DT 03-FEB-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1. .191
/*tag= a
192. .498
/*tag= b
499. .1187
/*tag= c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     595 TCCGGTCTTGCGCTCAG 611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    117 euArgGlyGlnSerGln 122
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338.50
3.319
73.381
                                                    alignment_block:
US-09-016-869A-6 x V53821
     Quality:
               Ratio:
Percent Similarity:
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aliqnment_block
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        400
    The present sequence represents part of intron 1, exon 2 and part of intron 2 for a human multiple tumour suppressor 1 (MTS1) gene. The MTS1 sequence is homologous to the corresponding murine gene. Primers designed from the gene can be used to design primers to detect abnormalities i.e. polymorphisms which may predispose towards malignancies such as melanoma, leukaemia, astrocytoma, lymphoma, glioma, as well as tumours of e.g. the breast, thyroid, pancreas, uterus and kidneys.

Sequence 1187 BP: 243 A; 354 C; 331 G; 255 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-MX-1996 (first entry)
Multiple tumour suppressor 1 (MTS1) cDNA.
Multiple tumour suppressor; MTS1; cancer; diagnosis; assay;
predisposition, melanoma; leukaemia; lymphoma; prognosis;
pancreas; breast; thyroid; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                    .........AsnValAlaGlnTh 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  495 TCAGGTGAGGACTGATGATCTGAGAATTTGTACYCTGAGAGCTTCCAAAG 544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             102 rAspGlyHisSerPheSerSer.....SerThrProArgAlaLeuGluL 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             345 GCGCGCCTGGACGTGCGGGATGCCTGGGGCCGTCTGCCCGTGGACCTGGC 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        445 GGGGCACCAGAGGCAGTAACCATGCCCGCATAGATGCCGCGGAAGGTCCC 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67
                                                                                                                                                                                                                                                                                                      1 MetMetMetGlyAsnValHisValAlaAlaLeuLeuLeuAsnTyrGlyAl 17
                                                                                                                                                                                                                                                                                                                                                             17 aAspSerAsnCysGluAspProThrThrPheSerArgProValHisAspA 34
                                                                                                                                                                                                                                                                                                                        51 AlaArgLeuAspValArgAspAlaTrpGlyArgLeuProLeuAspLeuAl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84 ysSerLeuCysSerAlaGlyTrpSerLeuCysThrAlaGly.....
                                                                                                                                                                        : 338.50 Length: 139
: 3.319 Gaps: 2
: 73.381 Percent Identity: 52.518
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/note= "splice site acceptor"
458
                                                                                                                                                                                                                                                                           to: 1187
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                                                                                                                                                                                                                                                                           from: 1
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T00747 standard; cDNA; 947 BP.
T00747;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCCGGTCTTGCGCTCAG 611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    euArgGlyGlnSerGln 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_name: N_Geneseq_36:T00747
                                                                                                                                                                                                                                 alignment_block:
US-09-016-869A-6 x V70585
                                                                                                                                                                                                                                                                         Align seg 1/1 to: V70585
                                                                                                                                                                          Quality:
Ratio:
                                                                                                                                                                                                   Percent Similarity
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                                                                                                                                                            alignment_scores
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Detecting polymorphism associated with cancer pre:disposition - also DNA, vectors and host cells e.g. for gene or protein replacement therapy and drug screening and drug screening. Disclosure; Pages 111-112; 148pp; English. An individual can be diagnosed as having a predisposition to cancer by detecting an alteration in the wild type multiple tumour suppressor (MTS) gene, using gene probes which hybridise to the MTS1 con a bove assay can also be used in the diagnosis and prognosis of melanoma, lymphoma, leukaemia and pancreas, breast and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84 ysSerLeuCysSerAlaGlyTrpSerLeuCysThrAlaGlyAsnValAla 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         196 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17 aAspSerAsnCysGluAspProThrThrPheSerArgProValHisAspA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MetMetMetGlyAsnValHisValAlaAlaLeuLeuLeuAsnTyrGlyAl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length: 122
Gaps: 2
Percent Identity: 57.377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       273 G;
                                                                                               18.MAR.1994; US-214582.
18.MAR.1994; US-215087.
18.MAR.1994; US-215086.
14.ARR-1994; US-227369.
01.JUN-1994; US-227369.
01.JUN-1994; US-251938.
(WYRL) WYRAAD GENETICS INC.
(UTAH ) UNIV UTAH RES FOUND.
Cannon-Albitght LA, Kamb A, Skolnick MH;
WPI; 95-344626/44.
/*tag= b
/note= "splice site acceptor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to: 947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         271 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Align seg 1/1 to: T00747 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       207 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_documentation_block:
ID T72311 standard; cDNA; 947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 480 GAGAGCCTCTGAGAAA 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          uArgGlyGlnSerGln 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Quality: 332.00
Ratio: 3.458
nilarity: 78.689
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cancers, etc
                                      WO9525813-A1.
28-SEP-1995.
17-MAR-1995; U03537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         947 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ratio:
Percent Similarity:
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67
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10-SEP-1997 (first entry)
Human multiple tumour suppressor gene 1.
Human; multiple; tumour; suppressor; MTS1; cancer; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84 ysSerLeuCysSerAlaGlyTrpSerLeuCysThrAlaGlyAsnValAla 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34 laAlaArgGluGlyPheLeuAspThrLeuValValLeuHisGlySerGly 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51 AlaArgLeuAspValArgAspAlaTrpGlyArgLeuProLeuAspLeuAl 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MetMetGlyAsnValHisValAlaAlaLeuLeuLeuAsnTyrGlyAl 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length: 122
Gaps: 2
Percent Identity: 57.377
                                                                                                                                                                                                                                                                                                                                                      Skolnick MH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          from: 1 to: 947
                                                                        Location/Qualifiers
1. .471
/*tag= a
                                                                                                                                                                                                                                       14-APR-1994; US-227369.
01-JUN-1994; US-251938.
17-MAR-1995; WO-U03537.
(MYRI-) MYRIAD GENETICS INC.
(UTAH ) UNIV UTAH RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quality: 332.00
Ratio: 3.458
Percent Similarity: 78.689
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                                                                                                                                                                                       US-214582.
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US-09-016-869A-6 x T72311
                                                                                                                                                                                                                                                                                                                                                                        WPI; 97-2582Ĭ7/23.
P-PSDB; W19251.
                                                                                                                                                                                                           18-MAR-1994;
18-MAR-1994;
                                                                                                                                                   29-APR-1997.
18-MAR-1994;
                                                                                                                                                                                       18-MAR-1994;
                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_scores:
                                                                                                                                  US5624819-A
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mutation(s) and their treatment to mislificate and mutation(s) and their treatment.

Disclosure; Column 89-90; 72pp; English.

This CDNA sequence encodes a variant of the human multiple tumour suppression protein, WTS1. The WTS gene locus is also referred to as the familial melanoma (MLM) gene locus, located on human chromosome 9p21.

Germ line mutations in MTS genes can be used in the diagnosis of predisposition to cancers, e.g. melanoma, leukaemia, astrocytoma, gliboblastoma, lymphoma, glioma, Hodgkin's lymphoma, CLL, and cancers of the pancreas, breast, thyrold, ovary, uterus, testis, kidney, stomach and rectum.
                                                                                                                                                                  15-JUL-1998 (first entry)
Human MTS1 cDNA variant.
MTS1; multiple tumour suppressor; diagnosis; cancer; germ-line mutation; familial melanoma locus; MLM; predisposition; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA specific for Multiple Tumour Suppressor 1E1-beta gene useful for the diagnosis of cancers related to MTS1E1-beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20
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|:::||| |||||||:::|||
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Gaps: 2
Percent Identity: 57.377
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                                                                                                                                                                                                                                                                                                                                                                                               /*tag= a
/note= "splice site acceptor"
458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag= b
/note= "splice site acceptor"
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                                                                                                                                                                                                                                                                                                                                                   ocation/Qualifiers
                                                      seq_documentation_block:

ID V11270; standard; cDNA; 947 BP.

V11270; bandard; cDNA, 947 BP.

DT 15-UUL-1998 (first entry)

E Human MTS1 cDNA variant.

WM MTS1; multiple tumour suppress

KW MTS1; multiple tumour suppress

FT MS2; multiple tumour suppress

FT WS2; MS2; MS2;

FT WS2; MS2; MS2;

FT WS2; MS2; MS2;

FT WS2; MS2; MS2;

FT WS2; MS2; WS2;

FT WS2; MS2; WS2;

FT WS2; MS2; WS2;

FT WS2; MS2;

FR WAR-1994; US-215086.

FR WAR-1994
                                                                                                        BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-JUN-1995; US-487033.

18-MAR-1994; US-214582.

18-MAR-1994; US-215086.

18-MAR-1994; US-215087.

14-ARR-1994; US-227369.

01-JUN-1994; US-227369.

17-MAR-1995; WO-U03316.

(MYRI-) MYRIAD GENETICS INC.
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seq_name: N_Geneseq_36:V11270
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Ratio: 3.458
Percent Similarity: 78.689
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US-09-016-869A-6 x V11270
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Mus musculus

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 339)

Santos,J., Melendez,B., Perez de Castro,I., Malumbres,M.,

Serrano,M., Pellicer,A. and Fernandez-Piqueras,J.

Comparative analysis of the pl6(INK4a) and pl5(INK4b) DNA sequences in mouse inbred strains

Unpublished

2 (bases I to 339)

Santos,J., Melendez,B., Perez de Castro,I., Malumbres,M.,

Serrano,M., Pellicer,A. and Fernandez-Piqueras,J.
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LOCUS MM079631 339 bp DNA ROD 05-JAN-1999
DEFINITION Mus musculus cyclin-dependent kinase inhibitor protein (p16(INK4a))
ACCESSION U79631
VERSION U79631.1 GI:4098149
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/product---cyclin-dependent kinase inhibitor protein"
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/db_xref="G1:4098148"
/translation="VaraMGNVHVAALLLNYGADSNCEDPTIFSRPVHDAAREGFLDTL
/translation="VaraMGRLPLDLAQERGHQDIVRYLRSAGSSLCSAGWSLCTAGNVAQ
TDGHSFSSSTP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54 AGATTCGAACTGCGAGGACCCCACTACCTTCTCCCGCCGGTGCACGACG 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       204 CCAAGAGCGGGACATCAAGACATCGTGCGATATTTGCGTTCCGCTGGGT 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67 aGlnGluArgGlyHisGlnAspIleValArgTyrLeuArgSerAlaGlyC 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34 laAlaArgGluGlyPheLeuAspThrLeuValValLeuHisGlySerGly 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 ATGATGATGATGACGAACGTTCACGTAGCAGCTCTTCTGCTCAACTACGGTGC 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17 aAspSerAsnCysGluAspProThrThrPheSerArgProValHisAspA 34
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Gaps: 0
Percent Identity: 98.214
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                                                                                                                                                                                                                                                                                       p
      <1. .>339
/gene="p16(INK4a)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                     579.00
5.216
99.107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ratio:
Percent Similarity:
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VERSION
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SOURCE
                                                                                                                                                                                                                                                                                BASE COUNT
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      CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Santos, J., Melendez, B., Perez de Castro, I., Malumbres, M., Serrano, M., Pellicer, A. and Fernandez-Piqueras, J. Comparative analysis of the p16(INK4a) and p15(INK4b) DNA sequences in mouse inbred strains
Unpublished
1 (Dases I to 339)
2 (Dases I to 339)
2 (Dases I to 339)
3 (Dases I to 339)
4 (Dases I to 339)
5 (Dases I to 339)
5 (Dases I to 339)
6 (Dases I to 339)
7 (Dases I to 339)
8 (Dase I to 339)

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LOCUS MMU79630 339 bp DNA ROD 05-JAN-1999
DEFINITION Was musculus cyclin-dependent kinase inhibitor protein (pl6(INK4a))
ACCESSION 079630
VERSION 079630.1 GI:4098147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 339)
                                                                                                                                                                                                                                                                                                                                                                                                        104 CAGCGCGGGAAGGCTTCCTGGACACGCTGCTGCTGCTGCTGCTCGCACGGTCAGGG 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84 ysSerLeuCysSerAlaGlyTrpSerLeuCysThrAlaGlyAsnValAla 100
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                                                                                                                                                                                                                                                34 laalaargGluGlyPheLeuAspThrLeuValValLeuHisGlySerGly 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51 AlaArgLeuAspValArgAspAlaTrpGlyArgLeuProLeuAspLeuAl 67
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                                                                                                                                                                                                                                                                                                                                                                           17 aAspSerAsnCysGluAspProThrThrPheSerArgProValHisAspA 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1. .339
/organism="Mus musculus"
/strain="c5/BL/6J, RF/J, and CAST/Ei"
/db_xref="taxon:10090"
/chromosome="4"
/map="between C3 and C6 bands"
Gaps: 0
Percent Identity: 98.214
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1. .339
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/number=2
                                                                                                                                                                                        from: 1
                                                                                                                                                                                  Align seg 1/1 to: MMU79633
5.252
99.107
                                                                                          alignment_block:
US-09-016-869A-6 x MMU79633
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                             Percent Similarity:
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AUTHORS
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us-09-016-869a-6.rge

JOURNAL

gene exon

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bands,
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                                                                                                                                                                                                                                                                                                                                                                                                  /chromosome="4"
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                                                                                                                                                                                                                                                                                                                                                                                                                                  <1. .>339
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1. .339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             113 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <1. .>339
/gene="p16(INK4a)"
/codon_start=1
   U79632.1 GI:4098151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /number=2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               578.00
5.207
99.107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_block:
US-09-016-869A-6 x MMU79632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_scores
   VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                      gene
                                                                                                                                                                                                                                                                                 JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        exon
                                                                                                         REFERENCE
                                                                                                                           AUTHORS
                                                                                                                                                                                             JOURNAL
                                                                                                                                                                                                                             AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDS
                                                                                                                                                                                                                                                                                                                  PEATURES
                                                                                                                                                                                                                                                               TITLE
                                                                                                                                                           TITLE
                                                                                                                                                                                                                                                                                                            /product="cyclin-dependent kinase inhibitor protein"
/protein_id="AAD00228.1"
/protein_id="AAD00228.1"
/b_xref="ci:4098150"
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VVLQGSGARLDVRDAWGRLPLDLAQERGHQDIVRYLRSAGSSLCSAGWSLCTAGNVAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_documentation_block:
LOCUS MMU79632 339 bp DNA ROD 05-JAN-1999
DEFINITION Mus musculus cyclin-dependent kinase inhibitor protein (p16(INK4a))
ACCESSION 079632
Direct Submission
Submitted (09-OCT-1996) Biologia, Universidad Autonoma de Madrid,
Cantoblanco, Madrid, Madrid 28049, Spain
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 204 CCAAGAGGGGGGACATCAAGACATCGTGCGATATTTGCGTTCCGCTGGGT 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84 ysSerLeuCysSerAlaGlyTrpSerLeuCysThrAlaGlyAsnValAla 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          254 cercrirererrececredererrirereracecredenacerece 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34 laalaargGluGlyPheLeuAspThrLeuValValLeuHisGlySerGly 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      aGlnGluArgGlyHisGlnAspIleValArgTyrLeuÀrgSerAlaGlyC 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 ATGATGATGATGAACGTTCACATAGCAGCTCTTCTGCTCAACTACGGTGC 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MetMetMetGlyAsnValHisValAlaAlaLeuLeuLeuAsnTyrGlyAl 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17 aAspSerAsnCysGluAspProThrThrPheSerArgProValHisAspA 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps: 0
Percent Identity: 97.321
                                                                                                                                                        /map="between C3 and C6 bands"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
                                                                                                                                                                                                                                                                                                                                                                                                                  73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to: MMU79631 from: 1 to: 339
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                                                                                                                                                                                                                                                                                                                                                                                                                111 9
                                                                                                                                                                                                            1. .339
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                                                                                                                                                                                                                                                                              /gene="p16(INK4a)"
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5.207
99.107
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US-09-016-869A-6 x MMU79631
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                  52
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29

BASE COUNT

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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Muss.
Eukheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

[ (bases 1 to 339)
Santos,J., Melendez,B., Perez de Castro,I., Malumbres,M.,
Serrano,M., Pellicer,A. and Fernandez-Piqueras,J.
Comparative analysis of the p16(INK4a) and p15(INK4b) DNA sequences
in mouse inbred strains
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="VMMMGNVHVAALLINYGADSNCEDPTTFSRPVHDAARGFLDTL
VVLQGSSGARLDVRDAWGRLPLDLAQERGHQDIVRYLRSAGWSLCSAGWSLCTAGNVAQ
TDGHSFSSSTP"
                                                                                                                                                                                                                                       2. (bases 1 to 339)
2. (bases 1 to 339)
Santos,J., Melendez,B., Perez de Castro,I., Malumbres,M.,
Serano,M., Pellicer,A. and Fernandez-Piqueras,J.
Direct Submission
Submistred (09-00T-1996) Biologia, Universidad Autonoma de Madrid,
Cantoblanco, Madrid, Madrid 28049, Spain
Location/Qualifiers
1. 339
/organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17 aAspSerAsnCysGluAspProThrThrPheSerArgProValHisAspA 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MetMetMetGlyAsnValHisValAlaAlaLeuLeuLeuAsnTyrGlyAl 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 ATGATGATGGGCAACGTTCACGTAGCAGCTCTTCTGCTCAACTACGGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length: 112
Gaps: 0
Percent Identity: 98.214
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204 GGAGCCCAACTGCGCCGACCCCGCCACTCTCACCCGACCCGTGCACGACG 253
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This is the nucleotide sequence of the invention. The MTS gene (MTS-1) gene, used in the method of the invention. The MTS gene (S susful in the diagnosis and prognosis of human cancer, e.g. by standard nucleic hybridistation techniques, of patient samples. The untated sequences are those that are present in sometic mutations of the gene in cancers. The vectors can be used for gene therapy strategies to replace function of mutated protein in patients. These can also be used to construct protein mimetics, also for therapoutic strategies. In addition the expression constructs can also be used for recombinant production of MTS. Recombinant MTS can be used to restrain a cerembinant production of MTS. Recombinant MTS can be used to screen for drugs to be used for cancer therapy, and the protein constructs of the protein cons
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acids based on multiple tumour suppressor, MTS, sequences useful as hybridisation probes, primers and recombinant production of MTS in the diagnosis and treatment of cancers related to MTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-DEC-1998 (first entry) coding sequence 3 of the multiple tumour suppressor 1. Multiple tumour suppressor 1, MTS-1; human; cancer; hybridisation; somatic mutation; gene therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                          84 ysSerLeuCysSerAlaGlyTrpSerLeuCysThrAlaGlyAsnValAla 100
                                                                                                                                                                                                                             101 GlnThrAspGlyHisSerPheSerSerSerThrProArgAlaLeuGluLe 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    documentation_block: V53851 standard; cDNA; 947 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (MYRI-) MYRIAD GENETICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             480 GAGAGCTCTGAGAAA 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           117 uArgGlyGlnSerGln 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-SEP-1998.

07-JUN-1995, 480810.

07-JUN-1995, US-480810.

18-MAR-1994, US-215086.

18-MAR-1994, US-215086.

18-MAR-1994, US-215087.

14-APR-1994, US-2215087.

01-JUN-1994, US-221389.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_name: N_Geneseq_36:V53851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kamb A;
WPI; 98-494842/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US5801236-A.
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Length: 122
Gaps: 2
Percent Identity: 57.377
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         Quality: 332.00
Ratio: 3.458
                                                             alignment_block:
US-09-016-869A-6 x V53851
                                    Percent Similarity:
alignment_scores:
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from: 1 to: 947 Align seg 1/1 to: V53851

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1 MetMetMetGlyAsnValHisValAlaAlaLeuLeuLeuAsnTyrGlyAl 17

```
design
Disclosure; Fig 17; 80pp; English.
Disclosure; Fig 17; 80pp; English.
The present sequence represents the cDNA sequence for a human multiple
The present sequence represents the cDNA sequence for a human. The gene
tumour suppressor 1 (MTS1) gene, including noncoding portions. The gene
can be used to design primers to detect abnormalities 1.e. polymorphisms
which may predispose towards malignancies such as melanoma, leukaemia,
aktrocytoma, lymphoma, glioma, as well as tumours of e.g. the breast,
thyroid, pencreas, uterus and kidneys.

commence 947 BP; 207 A; 271 C; 274 G; 195 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cDNA encoding a human multiple tumour suppressor 1 (MTS1) protein. Human; multiple tumour suppressor 1 gene; MTS1; cancer; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mouse multiple tumour suppressor gene segment - useful for primer
                                                                                                                                                                                                  84 ysSerLeuCysSerAlaGlyTrpSerLeuCysThrAlaGlyAsnValAla 100
                                                                 400 .........GCGGGGGCACC.....AGAGGCAGTAACCATGCC 429
                                                                                                                                                                                                                                                                     101 GlnThrAspGlyHisSerPheSerSerSerThrProArgAlaLeuGluLe 117
                               254 creccessassecrrecrssacaescrssrscrscrscrscrscsecesses 303
                                                                                                                                     84
                                                                                                                                 67 aGlnGluArgGlyHisGlnAspIleValArgTyrLeuArgSerAlaGlyC
Length: 122
Gaps: 2
Percent Identity: 57.377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag- a
/note- "splice site acceptor"
458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       b
"splice site acceptor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to: V70615 from: 1 to: 947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ВЪ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-JUL-1995; US-508735.
07-JUN-1995; US-487033.
(MYEL) MYRALD GENETICS INC.
Jiang P, Kamb A, Stone S;
WPI; 99-044585/04.
                                                                                                                                                                                                                                                                                                                                                                                                                               seq_documentation_block:
ID V70615 standard; cDNA; 947
AC V70615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-FEB-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                        480 GAGAGGCTCTGAGAAA 495
                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: N_Geneseq_36:V70615
                                                                                                                                                                                                                                                                                                                                    117 uArgGlyGlnSerGln 122
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3.458
78.689
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/note= "
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28-JUL-1995; 058735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       misc_feature
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1.0e-31
1.0e-31
1.0e-31
704.03
704.03
704.03
704.03
                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Stone, Steven
APPLICANT: Jiang, Ping
APPLICANT: Jiang, Ping
APPLICANT: Marb, Alexander
TITLE OF INVENTION: MTS GENE AND THERAPEUTIC USE THEREOF
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
332.00
332.00
332.00
332.00
                                                                                seq_name: /cgn2_6/ptodata/1/1na/5C_COMB.seq:US-08-508-735-44
                                                                                                                                                                                                                                                                         3: Venable, Baetjer, Howard & Civiletti,
1201 New York Avenue, Suite 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/508,735
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Splice site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US to be assigned FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION UNMBER: PCT/US95/03316
FILING DATE: 17-MAR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                          Sequence 44, Application US/08508735 Patent No. 5843756
                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: 126..127
OTHER INFORMATION: /note-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 507 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Quality: 658.00
Ratio: 5.264
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; LOCATION: 467..468
; OTHER INFORMATION:
US-08-508-735-44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                        CITY: Washington
                                                                                                             seq_documentation_block
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             õ
                                                                                                                                                                                                                                                                                                                                        USA
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                                                                                                                                                                                                                                                                                                                                                       20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HYPOTHETICAL:
                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_scores
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                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                       8.4e-72
8.4e-72
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 out_format : pfs
                                                              About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMB. seq: US-09-115-252-36 + 332.00
A.COMB. seq: US-08-115-252-36 + 332.00
A.COMB. seq: US-08-154-915-3 + 332.00
CTUS. COMB. seq: PCT-US93-09445-3 + 372.00
OM of: US-09-016-869A-6 to: Issued_Patents_NA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:PCT-US95-0
/cgn2_6/ptodata/1/ina/5A_COMB.seq:US-08-474-177
                                                                                                                                                                                                                                                                                                                                                                     Database: Issued_Patents_NA:*Database sequences: 243080
Database length: 68777915
Search time (sec): 85.310000
                               Date: Jul 21, 2000 8:07 AM
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Query: US-09-016-869A-6
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Align seg 1/1 to: US-08-534-975-1 from: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              117 uArgGlyGlnSerGlnGluGlnSer 125
                                                                                                                                                                                                                                                                                                                                                                US-09-016-869A-6 x US-08-534-975-1
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                 Quality: 658.00
Ratio: 5.264
Percent Similarity: 100.000
                                                                                                                43..548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: D.C.
COUNTRY: USA
                                                                                             NAME/KEY:
LOCATION:
FEATURE:
                                                                                                                                                  ; NAME/KEY:
; LOCATION:
US-08-534-975-1
                                                                                                                                                                                                                                                   alignment_scores:
                                                                                                                                                                                                                                                                                                                                              alignment_block:
                                                                           FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/08534975
Patent No. 572333
GENERAL INFORMATION:
APPLICANT: Sherr, Charles, J.
APPLICANT: Ouelle, Dawn, E.
TITLE OF INVENTION: ARF-p19, A No. 5723313el Regulator of the Mammalian Cell
TITLE OF INVENTION: Cycle
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
                                                                                                                                                                                                                         130 ATGATGATGGGCAACGTTCACGTAGCAGCTCTTCTGCTCAACTACGGTGC 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ysSerLeuCysSerAlaGlyTrpSerLeuCysThrAlaGlyAsnValAla 100
                                                                         1 MetMetMetGlyAsnValHisValAlaAlaLeuLeuLeuAsnTyrGlyAl 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_name: /cgn2_6/ptodata/1/ina/5B_COMB.seq:US-08-534-975-1
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COUNTRY: USA
ZIP: 20005
COMPUTER TEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM:
PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/534,975
FILING DATE: 28-SEP-1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
                                     to: 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUDRESSEE: Sterne, Ressler, Goldstein
STREET: 1100 New York Avenue Suite 600
CITY: Washington
                                     from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: FOX, Samuel, L.
REGISTRATION NUMBER: 30,353
REFERENCE/DOCKET NUMBER: 0656.0590000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 480 TCGCGGCCAATCCCAAGAGCAGAGC 504
                                     to: US-08-508-735-44
US-09-016-869A-6 x US-08-508-735-44
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seq_documentation_block:

; Sequence 1, Application US/08954470
; Patent No. 5876965;
; GENERAL INFORMATION:
; APPLICANT: Sherr, Charles, J.
; APPLICANT: Quelle, Dawn, E.
; TITLE OF INVENTION: ARF-p19, A No. 5876965el Regulator of the
; TITLE OF INVENTION: AMMORPHIAN Cell Cycle
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Avenue Suite 600
; CITY: Mashington
                                                                                                                                                                     485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              101 GlnThrAspGlyHisSerPheSerSerSerThrProArgAlaLeuGluLe 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17 aAspSerAsnCysGluAspProThrThrPheSerArgProValHisAspA 34
                                                                                                                                                 1 MetMetMetGlyAsnValHisValAlaAlaLeuLeuLeuAsnTyrGlyAl 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67 aGlnGluArgGlyHisGlnAspIleValArgTyrLeuArgSerAlaGlyC 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      436 CCAAGAGCGGGGACATCAAGACATCGTGCGATATTTGCGTTCCGCTGGGT
                                                                                                                                                                                                                                                                                                                       34 laAlaArgGluGlyPheLeuAspThrLeuValValLeuHisGlySerGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name: /cgn2_6/ptodata/1/ina/5C_COMB.seq:US-08-954-470-1
Percent Identity: 100.000
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117 uArgGlyGlnSerGlnGluGlnSer 125

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101 GlnThrAspGlyHisSerPheSerSerSerThrProArgAlaLeuGluLe 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84 ysSerLeuCysSerAlaGlyTrpSerLeuCysThrAlaGlyAsnValAla 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MetMetMetGlyAsnValHisValAlaAlaLeuLeuLeuAsnTyrGlyAl 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
CORPUTER: IEM PC compatible
CORPUTER: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/954,470
FILING DATE:
CLASSIFICATION: 0435
FILING DATE:
CLASSIFICATION: 08/534,975
FILING DATE:
RELECATION NUMBER: 08/534,975
FILING DATE:
REPLICATION NUMBER: 0656.0590000
TELECOMMUNICATION UNBER: 30,333
REFERENCE/DOCKET NUMBER: 0656.0590000
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 202-371-2600
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 713 base pairs
TYPE: NOCHOLIC COURSES: double
STRANDEDNES: double
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US-09-016-869A-6 x US-08-954-470-1
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Ratio: 5.264
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDS
43..548
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43..551
                                                                                                                                                                                                                                                                                                                                                                                                                                      unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY:
COCATION:
US-08-954-470-1
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    Sequence 1, Application US/09129855A
    Sequence 1, Application US/09129855A
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    APPLICANT: Sherr, Charles, J.
    APPLICANT: Quelle, Dawn, E.
    TITLE OF INVENTION: Cell Cycle
    NUMBER OF SEQUENCES: 12
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: Sterne, Kessler, Goldstein & Fox
    STREET: 1100 New York Avenue Suie 600
    CITY: Washington
    STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_name: /cgn2_6/ptodata/1/ina/6_COMB.seq:US-09-129-855A-1
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Percent Identity: 100.000
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/129,855A
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CLASSIFICATION: 435
PRIOR APPLICATION: DATA:
APPLICATION NUMBER: 08/954,470
FILING DATE: 20-CCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/534,975
FILING DATE: 27-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1340-1-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFRAX: 201-347-5800
TELEFRAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 713 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
586 TCGCGGCCAATCCCAAGAGCAGAGC 610
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US-09-016-869A-6 x US-09-129-855A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Quality: 658.00
Ratio: 5.264
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; LOCATION:
US-09-129-855A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
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213..587

us-09-016-869a-6.rni

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; LOCATION:
US-08-306-511A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Beach, David H.
APPLICANT: Demetrick, Douglas J.
APPLICANT: Serrano, Manuel
APPLICANT: Serrano, Manuel
APPLICANT: Hannon, Gregory J.
TITLE OF INVENTION: Cell-Cycle Regulatry Proteins, and Uses
TITLE OF INVENTION: Related Thereto
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 436 CCAAGAGCGGGGACATCAAGACATCGTGCGATATTTGCGTTCCGCTGGGT 485
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                    17 aAspSerAsnCysGluAspProThrThrPheSerArgProValHisAspA 34
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/306,511A
FILING DATE: 14-SEP-194
ATTONREY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REGISTRATION NUMBER: 36,709
TELEPRAM: (617) 227-7400
TELEPRAM: (617) 227-7400
TELEPRAM: (617) 227-541
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 853 base pairs
LENGTH: 813 base pairs
STRANDEDNESS: DOTH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_documentation_block:
    Sequence 5, Application US/08306511A
    Patent No. 5962316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: LAHIVE & COCKFIELD STREET: 60 State Street CITY: Boston STATE: MA COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: CDS
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84 ysSerLeuCysSerAlaGlyTrpSerLeuCysThrAlaGlyAsnValAla 100
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                                                                                                                                                                                                                                                                                                                                                                           34 laAlaArgGluGlyPheLeuAspThrLeuValValLeuHisGlySerGly 50
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    Sequence 5, Application US/08893274
    Patent No. 5968813
    GENERAL INFORMATION:
    APPLICANT: Beach, David H.
    APPLICANT: Berrano, Manuel
    APPLICANT: APPLICANT: Serrano, Manuel
    APPLICANT: Greapry J.
    TITLE OF INVENTION: Cell-Cycle Regulatory Proteins,
    TITLE OF INVENTION: and Uses Related Thereto
    NUMBER OF SEQUENCES: 10
    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_name: /cgn2_6/ptodata/1/ina/5D_COMB.seq:US-08-893-274-5
                                         Gaps: 0
Percent Identity: 100.000
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STREET: One Post Office Square
CITY: Boston
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/893,274
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          117 uArgGlyGlnSerGlnGluGlnSer 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   563 TCGCGGCCAATCCCAAGAGCAGAGC 587
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US-09-016-869A-6 x US-08-306-511A-5
                 Quality: 658.00
Ratio: 5.264
Percent Similarity: 100.000
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alignment_scores
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17 aAspSerAsnCysGluAspProThrThrPheSerArgProValHisAspA 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length: 125
Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Align seg 1/1 to: US-08-893-274-5 from: 1 to: 853
FILING DATE: 15-JULY-1997
CLASSIFICATION BATA:
APPLICATION NUMBER: US 08/306,511
FILING DATE: 14-SEPTEMBER-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/248,812
FILING DATE: 25-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,371
FILING DATE: 14-APRIL-1994
PRIOR APPLICATION DATA: 18-NOVEMBER-193
PRIOR APPLICATION DATA: 1994
PRIOR APPLICATION DATA: 18-NOVEMBER-193
PRIOR APPLICATION DATA: 1997
FILING DATE: 17-DECEMBER-192
PRIOR APPLICATION DATA: 17-DECEMBER-199
PRIOR APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-OCTOBER-1992
PRIOR APPLICATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: 36,709
REFERENCE/DOCKET NUMBER: 36,709
TELECOMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_block:
US-09-016-869A-6 x US-08-893-274-5
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Ratio: 5.264
Percent Similarity: 100.000
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213..587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
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; LOCATION:
US-08-893-274-5
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us-09-016-869a-6.rni

APPLICATION NUMBER: US 08/248,812 FILING DATE: 25-MAY-1994

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TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses TITLE OF INVENTION: Related Thereto NUMBER OF SEQUENCES: 10 COMPUTER READABLE FORM: MEDIUM TYPE: FIOPPy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                            17 aAspSerAsnCysGluAspProThrThrPheSerArgProValHisAspA 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67 aGlnGluArgGlyHisGlnAspIleValArgTyrLeuArgSerAlaGlyC 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                           34 laAlaArgGluGlyPheLeuAspThrLeuValValLeuHisGlySerGly 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51 AlaArgLeuAspValArgAspAlaTrpGlyArgLeuProLeuAspLeuAl 67
                                                                                                                                                                                                                                                                                                        1 MetMetMetGlyAsnValHisValAlaAlaLeuLeuLeuAsnTyrGlyAl 17
                                                                                                                                                                      Percent Identity: 100.000
                                                                                                                                                                                                                                                                   Align seg 1/1 to: US-08-581-918A-5 from: 1 to: 853
                                                                                                                                                        Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILLING CONTROL CARACTERIST CATION:
PRIOR APPLICATION NUMBER: US 08/346,147
PILING DATE: 29-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/306,511
**TITNG DATE: 14-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_documentation_block:
; Sequence 5, Application PC/TUS9504636
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             117 uArgGlyGlnSerGlnGluGlnSer 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  563 TCGCGGCCAATCCCAAGAGCAGAGC 587
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US-09-016-869A-6 x US-08-581-918A-5
                                                                                                                                                      Ratio: 5.264
Percent Similarity: 100.000
                                                                                                                                    658.00
                       CDS
213..587
                                                                                                                                    Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                   ; NAME/KEY:
; LOCATION:
US-08-581-918A-5
                                                                                                                alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
FEATURE:
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seq_documentation_block:
    Sequence 5, Application US/08627610
    Sequence 5, Application US/08627610
    Patent No. 5919997
    GENERAL INFORMATION:
    APPLICANT: Beach, David H.
    APPLICANT: Serrano, Manuel.
    APPLICANT: Derinho, Ronald A.
    TITLE OF INVENTION: Transgenic Animals Having Modified Cell-Cycle
    TITLE OF INVENTION: Regulation
    NUMBER OF SEQUENCES: 13
    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84 ysSerLeuCysSerAlaGlyTrpSerLeuCysThrAlaGlyAsnValAla 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17 aAspSerAsnCysGluAspProThrThrPheSerArgProValHisAspA 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   463 GCTCTTTGTGTTCCGCTGGGTGTCTTTGTGTACCGCTGGGAACGTCGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34 laAlaArgGluGlyPheLeuAspThrLeuValValLeuHisGlySerGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_name: /cgn2_6/ptodata/1/ina/5D_COMB.seq:US-08-627-610-5
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Gaps: 0
Percent Identity: 100.000
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   FILING DATE: 14-APR-1994
; INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 853 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             117 uArgGlyGlnSerGlnGluGlnSer 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to: PCT-US95-04636-5
                                                                                                                                                                                                                                                                                                                                                                                     alignment_block:
US-09-016-869A-6 x PCT-US95-04636-5
                                                                                                                                                                                                                                                                                                           Quality: 658.00
Ratio: 5.264
Percent Similarity: 100.000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: (
                                                                                                                                                                                                     CDS
213..587
                                                                                                                                                               MOLECULE TYPE: CDNA
                                                                                                                                                                                                   ; NAME/KEY:
; LOCATION:
PCT-US95-04636-5
                                                                                                                                                                                                                                                                                              alignment_scores:
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GENERAL INFORMATION:
APPLICANT: Skolnick, Mark H.
APPLICANT: Cannon-Albright, Lisa A.
APPLICANT: Cannon-Albright, Lisa A.
APPLICANT: Cannon-Albright, Lisa A.
APPLICANT: Cannon-Albright, Lisa A.
APPLICANT: Cannon-Albright B.
ITLE OF INVENTION: GERMINE MUTATIONS IN THE MTS GENE
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Sulte 1000
CITY: Washington
STATE: DC
COUNTRY: USA
                                                                                                                                                          seq_name: /cgn2_6/ptodata/1/ina/5A_COMB.seq:US-08-474-177-25
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Gaps: 0
Percent Identity: 98.824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Ralease #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,177
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FILING DATE: 07-JUN-1995
CLASSIFICATION: 4355
PIGOR APPLICATION NUMBER: DCT/US95/03537
FILING DATE: 17-MAR-1995
FILING DATE: 17-MAR-1995
FILING DATE: 17-MAR-1995
FILING DATE: 10-JUN-1994
FILING DATE: 01-JUN-1994
FILING DATE: 18-MAR-1994
FILING DATE: 18-MAR-1994
FILING DATE: 18-MAR-1994
FILING DATE: 18-MAR-1994
FILING DATE: 14-APR-1994
FILING DATE: 14-APR-1994
FILING DATE: 14-APR-1994
FILING DATE: 14-APR-1994
FILING DATE: 18-MAR-1994
seq_documentation_block:
; Sequence 25, Application US/08474177
; Patent No. 5624819
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 395 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouality: 445.00
Ratio: 5.235
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84 ysSerLeuCysSerAlaGlyTrpSerLeuCysThrAlaGlyAsnValAla 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  101 GlnThrAspGlyHisSerPheSerSerThrProArgalaLeuGluLe 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    508 CAGACGACGGCATAGCTTCAGCTCAAGCACGCCCAGGGCCCTGGAACT 557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              308 CAGCGCGGGAAGGCTTCCTGGACACGCTGGTGGTGCTGCACGGGTCAGGG 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34 laAlaArgGluGlyPheLeuAspThrLeuValValLeuHisGlySerGly 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MetMetGlyAsnValHisValAlaAlaLeuLeuLeuAsnTyrGlyAl 17
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Percent Identity: 100.000
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                                                                                                                                                      ZIP: 02109

COMPUTER: USA
ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURENT APPLICATION DATA:
APPLICATION WHRER: US/08/627,610
FILING DATE: 04-APR-1996
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REGISTRATION INFORMATION:
TELEFONE: (617) 227-7400
TELEFONE: (617) 227-7401
   ADDRESSEE: LAHIVE & COCKFIELD STREET: 60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_block:
US-09-016-869A-6 x US-08-627-610-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouality: 658.00
Ratio: 5.264
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                           Boston
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; NAME/KEY: ; LOCATION: US-08-627-610-5

alignment_scores:

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190 AGATTCGAACTGCGAGGACCCCACTACCTTCTCCCGCCGGGGCACGACG 239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      240 CAGCGCGCGAAGGCTTCCTGGACACGCTGGTGGTGCTGCTGCAGGGTCAGGG 289
                                                                                                                                                                                                                                                                                                                                                                  34 laAlaArgGluGlyPheLeuAspThrLeuValValLeuHisGlySerGly 50
                                                                                                                                                                                                                                                       17 aAspSerAsnCysGluAspProThrThrPheSerArgProValHisAspA 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51 AlaArgLeuAspValArgAspAlaTrpGlyArgLeuProLeuAspLeuAl 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Kamb, Alexander
TITLE OF INVENTION: MTSIE1-Beta GENE
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name: /cgn2_6/ptodata/1/ina/5B_COMB.seq:US-08-487-033-25
                                                                                                                                           1 MetMetGlyAsnValHisValAlaAlaLeuLeuLeuAsnTyrGlyAl
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CIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,033
FILING DATE: 07-JUN 1995
CLASSIFICATION DATA:
APPLICATION NUMBER: DCT/US95/03316
FILING DATE: 17-MAR-1995
PRIOR APPLICATION NUMBER: US 08/251,938
FILING DATE: 01-JUN-1994
PRIOR APPLICATION NUMBER: US 08/251,938
FILING DATE: 18-MAR-1994
PRIOR APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-MAR-1994
PRIOR APPLICATION NUMBER: US 08/215,086
FILING DATE: 18-MAR-1994
PRIOR APPLICATION NUMBER: US 08/227,369
FILING DATE: 14-MAR-1994
PRIOR APPLICATION NUMBER: US 08/227,369
FILING DATE: 14-MAR-1994
PRIOR APPLICATION NUMBER: US 08/227,369
FILING DATE: 14-MAR-1994
PRIOR APPLICATION NUMBER: US 08/214,582
APPLICATION NUMBER: US 08/214,582
APPLICATION NUMBER: US 08/214,582
                                                                                       from: 1 to: 395
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FILING DATE: 18-MAR-1994
ATTORNEY/AGENT INFORWATION:
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Patent No. 5739027
GENERAL INFORMATION:
                                                                                    Align seg 1/1 to: US-08-474-177-25
alignment_block:
US-09-016-869A-6 x US-08-474-177-25
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STATE: DC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
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290 geredecredargredecardecredegredecredecredaerrede 339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP STREET: 1201 New York Avenue, Suite 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_name: /cgn2_6/ptodata/1/ina/5B_COMB.seq:US-08-480-810-25
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                                                                                                                                                                                                                                                                                                                                                        Length: 85
Gaps: 0
Percent Identity: 98.824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patentin Release #1.0, Version #1.30
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCETORET NUMBER: 24884-109348-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to: US-08-487-033-25
                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_block:
US-09-016-869A-6 x US-08-487-033-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Kamb, Alexander
ITILE OF INVENTION: MTS1 GENE
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
                                                                                                                                                 LENGTH: 395 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                           Ratio: 5.235
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Washington
                                                                                                                                                                                                                                                                                                                                                            Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         390 GCTCT 394
                                                                                                                                                                                                                                                                 ; ANTI-SENSE:
US-08-487-033-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84 ysSer 85
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seq_documentation_block:

Sequence 25, Application US/08508735

Patent No. 5843756

APPLICANT: Stone, Steven

APPLICANT: Stone, Steven

APPLICANT: Ramb, Alexander

TITLE OF INVENTION: WTS GENE AND THERAPEUTIC USE THEREOF

NUMBER OF SEQUENCES: 47

CORRESPONDENCE ADDRESS:

ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP

STREET: 1201 New York Avenue, Suite 1000

CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34 laAlaArgGluGlyPheLeuAspThrLeuValValLeuHisGlySerGly 50
                                                        seq_name: /cgn2_6/ptodata/1/ina/5C_COMB.seq:US-08-508-735-25
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MEDIUM TYPE: CIOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/508,735
FILING DATE:
APPLICATION NUMBER: US to be assigned
FILING DATE: 07-JUN-1995
PRIOR APPLICATION NUMBER: PCT/US95/03316
FILING DATE: 17-MAR-1995
ATTING DATE: 17-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 24884-109348
TELECOMMUNICATION INFORMATION:
METERPONE: 202-962-4848
TELECHOME: 202-962-4848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            oaps: 0
Percent Identity: 98.824
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US-09-016-869A-6 x US-08-508-735-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 395 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality: 445.00
Ratio: 5.235
Percent Similarity: 100.000
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
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ZIP: 20005
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MOLECULE TYPE:
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               390 GCTCT 394
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US-08-508-735-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               240 CAGCGCGCGAAGGCTTCCTGGACACGCTGGTGGTGCTGCTGCACGGTCAGGG 289
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Percent Identity: 98.824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to: US-08-480-810-25 from: 1 to: 395
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,810
CLASSIFICATION: 435
CLASSIFICATION: 435
CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNHBER: PCT/US95/03316
FILING DATE: 17-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,938
FILING DATE: 01-JUN-1994
PRIOR APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-MAR-1994
PRIOR APPLICATION NUMBER: US 08/215,086
FILING DATE: 18-MAR-1994
PRIOR APPLICATION NUMBER: US 08/214,582
FILING DATE: 14-APR-1994
PRIOR APPLICATION NUMBER: US 08/214,582
FILING DATE: 14-APR-1994
APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-MAR-1994
ATTORNEX/AGENT INFORMATION:
NAME: Inhen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 28,957
TELEPHONE: 202-962-4810
TELEPHONE: 202-962-4810
INFORMATION FOR SEO ID NO: 25:
FEQUENCE CHARACTERISTICS:
FEGUENCE CHARACTERISTICS:
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US-09-016-869A-6 x US-08-480-810-25
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TYPE: nucleic acid
STRANDEDNESS: double
OTHERSES: Ilnear
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Ratio: 5.235
Percent Similarity: 100.000
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HYPOTHETICAL:

US-08-480-810-25

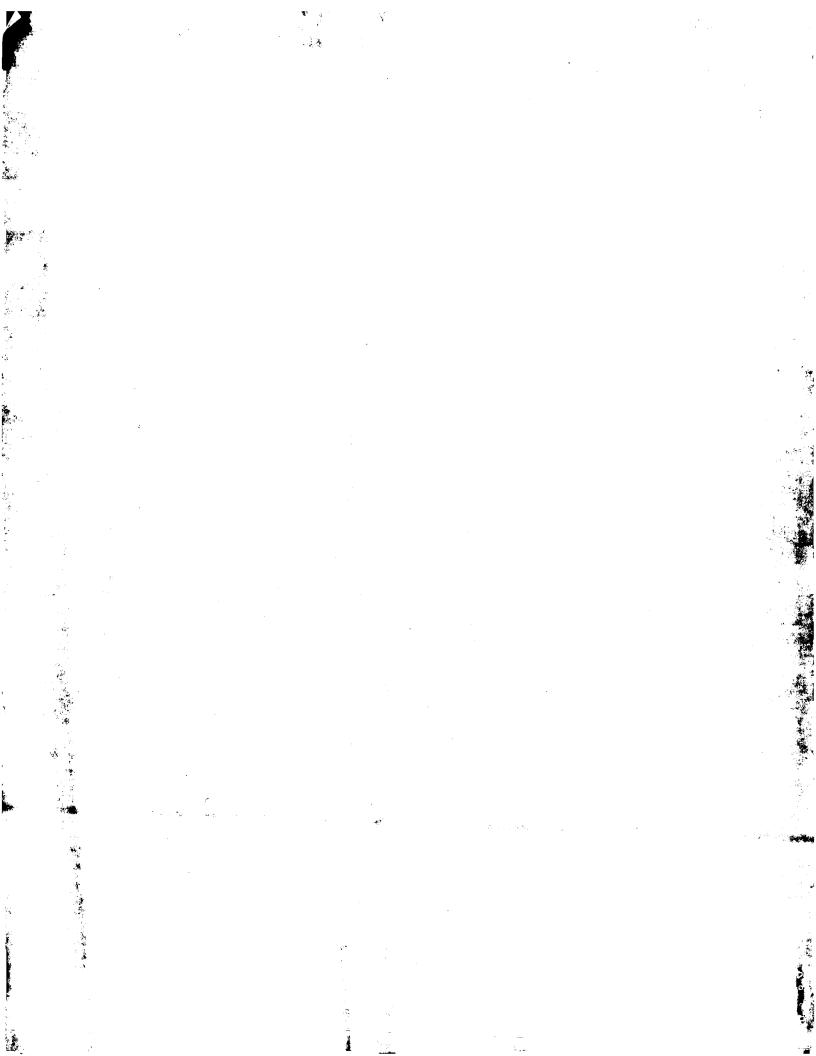
alignment_scores:

from: 1 to: 395

84 ysSer 85

Length:

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    Sequence 25, Application US/08486047
    Patent No. 5944095
    GENERAL INFORMATION:
    APPLICANT: Kamb, Alexander
    TITLE OF INVENTION: MTS2 GENE
    TUMBER OF SEQUENCES: 36
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
    STREET: 1201 New York Avenue, Suite 1000
    CITY: Washington
    CITY: Washington
    STATE: DC
    COUNTRY: USA
    ZIP: 20005
    CONPUTER PEADABLE FORM:
    CONPUTER PEADABLE FORM:
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                                                                                                                                                                                                                                                                                                                         Percent Identity: 98.824
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,047
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
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APPLICATION NUMBER: PCT/US95/03316
FILIND DATE: 17-MAR-1995
PRIOR APPLICATION DATA:
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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US-09-016-869A-6 x US-08-848-251-25
LENGTH: 395 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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                                                                                                 MOLECULE TYPE: CDNA
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HYPOTHETICAL:
ANTI-SENSE:
US-08-848-251-25
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Sequence 25, Application US/08848251
Patent No. 5989815
GENERAL INFORMATION:
APPLICANT: Skolnick, Mark H.
APPLICANT: Skolnick, Mark H.
APPLICANT: Gannon-Albright, Lisa A.
APPLICANT: General CENTION: GENERINE MUTATIONS IN THE MTS GENE AND TITLE OF INVENTION: METHOD FOR DETECTING PREDISPOSITION TO CANCER AT THE MTS TITLE OF INVENTION: GENERAL CENTION TO CANCER AT THE MTS OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
                                                                                                    240 CAGCGCGCAAGGCTTCCTGGACACGCTGGTGGTGCTGCACGGGTCAGGG 289
                                                                                                                                                                                                                                                                                                                                                                          seq_name: /cgn2_6/ptodata/1/ina/5D_COMB.seq:US-08-848-251-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
CITY: Washington
                                                                       51 AlaArgLeuAspValArgAspAlaTrpGlyArgLeuProLeuAspLeuAl
  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/848,251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24884-109348-G
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CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION NUMBER: US 08/474,083
FILING DATE: 07-JUN 1995
APPLICATION NUMBER: PCT/US95/03537
FILING DATE: 17-MAR-1995
PRIOR APPLICATION NUMBER: US 08/251,938
FILING DATE: 01-JUN 1994
PRIOR APPLICATION NUMBER: US 08/251,938
FILING DATE: 01-JUN 1994
PRIOR APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-MAR-1994
PRIOR DATE: 18-MAR-1994
PRIOR APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-MAR-1994
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FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,369
FILING DATE: 14-APR-1994
PRIOR APPLICATION NUMBER: US 08/214,582
APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-MAR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Ihnen, Jeffrey L. REGISTRATION NUMBER: 28,957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 24
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
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NCI_CGAP SOares m NCI_CGAP

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalais; Butheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 590)

NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NAtional Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/PBTGAP), Tumor Gene Index
Unpublished (1998)
On Oct 30, 1998 this sequence version replaced g1:3813427.
Contact: Robert Strausberg@nlh.gov
                                                                                                                                                                    A1871381 590 bp mRNA EST 07-MAR-2000 w181d11.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2431317 3' similar to TR:Q16361 Q16361 CELL CYCLE NEGATIVE REGULATOR BETA FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequencing Center
information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: Robert_Strausberg@nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
  wd93c07.x1
mj40b12.r1
w150c04.x1
qk47d01.x1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
  AI703354 v
AA051335 n
AI869175 v
AI280899 q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bonaldo, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

CDNA Sequencing by: Washington University Genome Seq

Clone distribution: NCI-CGAP clone distribution inf
found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html
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Seq primer: -400F from Glbco

High quality sequence stop: 444.

Location/Qualifiers
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Gaps: 2
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US-09-016-869A-6 x AI871381/rev
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AI871381
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Ratio:
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gb_est24:AI703354
gb_est1:AA051335
gb_est26:AI869175
gb_est18:AI280899
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                                                                                                                                                                                                                                                                                                                     SOURCE
ORGANISM
                                                                                                                                                                                                                                                     ACCESSION
VERSION
KEYWORDS
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TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             out_format : pfs
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gb_est26:AI871381
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LOCUS AI394605
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                                                           127
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LOCUS AW328496 648 bp mRNA EST 28-JAN-2000
DEFINITION ds02h12.x1 NIH_MGC_4 Homo sapiens cDNA clone IMAGE:2847599 5', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 648)
NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
National institutes of Health, Mammalian Gene Collection (MGC)
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/lab_host="Drgan: Cervix; Vector: pOTB7a; Site_1: SceI;
Site_2: CeuI; DoNA made by Oligo-dr priming.
Directionally cloned into CeuI/SceI sites using the
following 5' adaptor: taactataacggtcctaaggtagcga and 3'
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On Apr 7, 1998 this sequence version replaced gi:3036295.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-153
Email: Robert_Strausberg@nih.gov
Tissue Procurement: ATC
CONA Library Preparation: Edge BioSystems
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing Center (NISC)
Clone distribution: MGC Clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                            84 ysSerLeuCysSerAlaGlyTrpSerLeuCysThrAlaGlyAsnValAla 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GlnThrAspGlyHisSerPheSerSerThrProArgAlaLeuGluLe 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             284 CGCATAGATGCCGCGGAAGGTCCCTCAGACATCCCCGATTGAAAGAACCA 235
                 560 ATGATGATGGGCAGCGCCAGAGTGGCGGAGCTGCTGCTGCTCCACGGCGC 511
                                                                                                                                                                                                                         51 AlaArgLeuAspValArgAspAlaTrpGlyArgLeuProLeuAspLeuAl 67
                                                                                                                                                                                                                                                                                                        67 aGlnGluArgGlyHisGlnAspIleValArgTyrLeuArgSerAlaGlyC 84
                                                                                                                                                                                                                                                                                                                                                                                                                   34 laAlaArgGluGlyPheLeuAspThrLeuValValLeuHisGlySerGly
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Plate: LLCM0030 row: 0 column: 24
Seq primer: -21M13 forward primer (ABI)
Location/Qualifiers
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sequence.
AW328496
AW328496.1 GI:6798992
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234 GAGAGGCTCTGAGAAA 219
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tg13g05.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2108696 3'
sinilar to SW.CDN2_HUMAN P42771 CYCLIN_DEPENDENT KINASE 4 INHIBITOR
A ; contains LTR9.b3 TAR1 repetitive element ;, mRNA sequence.
A1394605.1 GI:4224152
adaptor: tttcattacctctttctccgcaccccacataaa. Average insert size 900 bp. Library prepared by Edge BioSystems
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 566)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP).
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Tissue Procurement: Ash Alizadeh, John Byrd, M.D., Mike Grever,
M.D., Louis M. Staudt, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         360
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Email: Robert_Strausberg@nih.gov
                                                                   ρ
                                                                   196
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FEATURES
                                                                                                                       cDNA Library Preparation: M. Bento Soares, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Greg Lennon, Ph.D. DNA Sequencing Dy: Washington University Genome Sequencing Center Clone distribution information and found through the I.M.A.G.E. Consortium/LLNL at: Insert Length: 755 Std Error: 0.00 Seq primer: -400P from Gloco High quality sequence stop: 457.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       297
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Gaps: 2
Percent Identity: 56.557
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                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_block:
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Percent Similarity:
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1 (bases 1 to 579)

NCI/NINDS-CGAP http://www.ncbi.nlm.nlh.gov/ncicgap.
National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index

Unpublished (1998)

On May 18, 1998 this sequence version replaced gl:3136859.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550

Email: Robert_Strausberg@nih.gov
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CDNA Library Arrayed by: Greg Lennon, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-GAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

Www-bio.lnl.gov/bbrp//lmage.html

Insert Length: 819 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 474.
Email: Robert_Strausberg@nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
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Percent Identity: 56.557
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                                                                                                                                                                                . mRNA sequence.
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SOURCE
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ORIGIN
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Constitution of the property o
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similar to TR:Q13195 Q13195 P16INK4/MTS1. (2) TR:Q13399 ;contains
LTR9.b3 TAR1 repetitive element ;, mRNA sequence.
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10 (bases 1 to 708)
10 (NCI/NINDS-CAPP http://www.ncbi.nlm.nth.gov/ncicgap.
10 National Cancer Institute / National Institute of Neurological National Cancer Institute / National Institute of Neurological National Cancer Institute / National Institute of Neurological Object (CGAP/PRGAP), Tumor Gene Index Unpublished (1998)
10 National Cancer Strausberg, Ph.D.
11 (301) 496-1550
12 Email: Robert_Strausberg@nih.gov
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                                         84 ysSerLeuCysSerAlaGlyTrpSerLeuCysThrAlaGlyAsnValAla 100
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34 laAlaArgGluGlyPheLeuAspThrLeuValValLeuHisGlySerGly
                                                                                                                                                                          51 AlaArgLeuAspValArgAspAlaTrpGlyArgLeuProLeuAspLeuAl
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/lab_nost="PH10B"
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/db_xref="taxon:9606"
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AI363262.1 GI:4114883
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seq_documentation_block:
LOCUS AI198233 579 bp mRNA EST 02-DEC-1998
DEFINITION q155412.11 NCI_CGAP_BRID5 Home sapiens cDNA clone IMAGE:1860407 3'
Similar to TR:Q16361 Q16361 CELL CYCLE NEGATIVE REGULATOR BETA FORM
CONTAINS LTR9.b3 TAR1 TAR1 repetitive element ;, mRNA sequence.
    and cloned into
adaptors (Pharmacia), digested with Not I and cloned int the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized, and was constructed by Bento Soares and M.Fatima Bonaldo."

210 c 219 g 140 t 2 others
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NCI/NTNDS-GAP http://www.ncbl.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurological Josofders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/PBTGAP), Tumor Gene Index
Unpublished (1998)
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Gaps: 2
Percent Identity: 56.557
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Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                          to reverse of: AI363262
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US-09-016-869A-6 x AI363262/rev
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3.400
77.869
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Ratio:
Percent Similarity:
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On Dec 15, 1999 this sequence version replaced gi:4575297.
Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3887
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
library availablility, please contact Piter de Jong
(pleter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@tesgen.com). BAC end Web Server:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo saplens"
/db_xref="taxon.9606"
/clone="late=651 Col=23 Row=K"
/clone=lib="Ref_1" Human Male BAC Library"
/sex="male"
/note="vector: pBACe3.6; Site_1: EcoR1; Site_2: EcoR1;
Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoR1 and EcoR1 Methylase. Size selected DNA was cloned into the BBACe3.6 vector at EcoR1 Sites
182 c 171 g 133 t 11 others
                                                                                                                                                                                                                                                                          Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 614)
Mahalras, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
                                                                                                                                                                                                                                                                                                                                                                                               Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
                                                                                                AQ496105 614 bp DNA GSS 28-APR-1999 HS_5075_A1_F12_T7 RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate-651 Col-23 Row-K, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                    Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
99380589
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Gaps: 0
Percent Identity: 72.840
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Plate: 651 row: K column: 23
Seq primer: T7
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Location/Qualifiers
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    223 GAGAGGCTCTGAGAAA 208
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US-09-016-869A-6 x AQ496105
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                                         seq_name: gb_gss7:AQ496105
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                                                                                seq_documentation_block:
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                               TITLE
                                                 T 3/]; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into Library is normalized, and was constructed by Bento Soares and M.Fatima Bonaldo."
fissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
                                    cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     101 GlnThrAspGlyHisSerPheSerSerSerThrProArgAlaLeuGluLe 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         273 CGCATAGATGCCGCGGAAGGTCCCTCAGACATCCCCGATTGAAAGAACCA 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84 ysSerLeuCysSerAlaGlyTrpSerLeuCysThrAlaGlyAsnValAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MetMetMetGlyAsnValHisValAlaAlaLeuLeuAsnTyrGlyAl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67 aGlnGluArgGlyHisGlnAspIleValArgTyrLeuArgSerAlaGlyC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps: 2
Percent Identity: 55.738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to reverse of: AI198233 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     177 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_block:
US-09-016-869A-6 x AI198233/rev
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    315.00
3.351
77.049
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_scores:
Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          113
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ORIGIN
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                                                                                                                                                                                                                                     FEATURES
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17

to: 774

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Bonaldo, Ph.D. cDN Library Arrayed by: Greg Lennon, Ph.D. cDN Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www.bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_documentation_block:

LOCUS AI362049 580 bp mRNA EST 15-FEB-1999

DEFINITION qy39f07.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2014405 3'

Similar to TR:Q16361 Q16361 CELL CYCLE NEGATIVE REGULATOR BETA FORM

', mRNA sequence.

ACCESSION AI362049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleoston Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (Dases 1 to 580) NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. Disorders and Stroke, Brain Tumor. Genome Anatomy Project (CGAP/BRGAP), Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     584 ATGATGATGGCCAGCGCCCGAGTGGCGGAGCTGCTGCTGCTCCACGGCGC 535
                                                                                                                                                                                                                                                                                                                                                                                534 GGAGCCCAATTGGGCCGACCCCGCCACTTTCACCCGAACCGTGCACGACG 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100 AlaGlnThrAspGlyHisSerPheSerSerSerThrProArgAlaLeuGl 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       311 GCCCGCATAAATGCCGCGGAAGGTCCCTCAGACATCCCCGATTTAAAGAA 262
                                                                                                                                                                                                                                                                                                                         17 aAspSerAsnCysGluAspProThrThrPheSerArgProValHisAspA 34
                                                                                                                                                                                                                                                                                                                                                                                                                                       34 laAlaArgGluGlyPheLeuAspThrLeuValValLeuHisGlySerGly 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cDNA Library Preparation: M. Bento Soares, Ph.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67 aGlnGluArgGlyHisGlnAspIleValArgTyrLeuArgSerAlaGlyC 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84 ysSerLeuCysSerAlaGlyTrpSerLeuCysThrAlaGly...AsnVal 99
                                                                                                                                                                                                         1 MetMetMetGlyAsnValHisValAlaAlaLeuLeuLeuAsnTyrGlyAl
Percent Identity: 57.500
                                                                                                                                                  from: 1
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Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seq primer: -40UP from Gibco
                                                                                                                                               Align seg 1/1 to reverse of: AI765096
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                                                      alignment_block:
US-09-016-869A-6 x AI765096/rev
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75.833
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           261 CCAAAGAGGG 252
Percent Similarity:
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COMMENT
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KEYWORDS
SOURCE
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Subtraction by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
Glound through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 854 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 400.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A170509 W18 NCI_CGAP_COL Homo sapiens cDNA clone IMAGE:2393463 3/
similar to TR:Q13399 Q13399 HYPOTHETICAL 18.1 KDA PROTEIN ; contains
LTR9.b3 MER22 repetitive element ;, mRNA sequence.
A1765096.1 GI:5231605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 774)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
On Feb 22, 1999 this sequence version replaced gi:4283180.
Contact. Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       fissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck
                                                                                                                                               446
                                                                                                                                                                                                                                                                   447 GCGCGGCTGGACGTGCGCTATGCCTGGGGCCGTCTGCCCGTGGACCTGGC 496
                                                                                                                                                                                                         67
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                                                                                  51 AlaargLeuAspValargAspAlaTrpGlyArgLeuProLeuAspLeuAl
                                                                                                                                                                                                                                                                                                                                                        aGlnGluArgGlyH1sGlnAspIleValArgTyrLeuArgSer 81.
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Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             774 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_name: gb_est25:AI765096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_documentation_block:
LOCUS A1765096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality:
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uman.

ORGANISM

REFERENCE AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

DEFINITION

67

ACCESSION VERSION KEYWORDS SOURCE M. Fatima

alignment_scores:

BASE COUNT ORIGIN

FEATURES

BASE COUNT

ORIGIN

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Bonaldo, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

CDNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

WWW-bio.llnl.gov/bbrp/lmage.html
Insert Length: 626 Std Error: 0.00

High quality sequence stop: 465.

Location/Qualifiers
                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 528)
NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. Mitional Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: Robert_Strausbergenih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1. .528
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58 AlaTrpGlyArgLeuProLeuAspLeuAlaGlnGluArgGlyH1sGlnAs 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Align seg 1/1 to reverse of: AI885362 from: 1 to: 528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Identity: 57.391
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US-09-016-869A-6 x AI885362/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3.483
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                                                                                                                                             Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            106
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                                                                                                                                          ORGANISM
                                                                                                                                                                                                                               REFERENCE
AUTHORS
TITLE
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COMMENT
                                                                                 KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US AI885362 528 bp mRNA EST 07-MAR-2000 101 M192h04.X1 NCI_CGAP_Brn25 Homo sapiens CDNA clone IMAGE:2432407 3 Similar to SW:CDN2_HUMAN P42771 CYCLIN-DEPENDENT KINASE 4 INHIBITOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MetMetMetGlyAsnValHisValAlaAlaLeuLeuLeuAsnTyrGlyAl 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84 ysSerLeuCysSerAlaglyTrpSerLeuCysThrAlaglyAsnValAla 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     304 ......GCGGGGGCACC.....AGAGGCAGTAACCATGCC 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               101 GlnThrAspGlyHisSerPheSerSerSerThrProArgAlaLeuGluLe 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Align seg 1/1 to reverse of: Al362049 from: 1 to: 580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length: 122
Gaps: 2
Percent Identity: 54.918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
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High quality sequence stop: 321.
Location/Qualifiers
1. 580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_block;
US-09-016-869A-6 x AI362049/rev
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3.309
77.049
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  224 GAGAGGCTCTGAGAAA 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_name: gb_est26:A1885362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seg_documentation_block:
)CUS AI885362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_scores:
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us-09-016-869a-6.rst
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alignment_block:
uS-09-016-869A-6 x AI817709/rev
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120 nSerGln 122
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                                                                                                                                         Align seg 1/1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing of Clone distribution: NCI-CGAP Clone distribution in NCI-CGAP Clone distribution in NCI-CGAP Clone distribution: NCI-CGAP Clone distribution in NCI-CGAP Clone distribution can be close distribution can be close distribution in NCI-CGAP Clone distribution can be close distribution in NCI-CGAP Clone distribution can be close distribution in NCI-CGAP Clone distribution can be close distributio
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Matazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukeryota; Mamalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Manalia; Lo 729)

1 (bases 1 to 729)

1 (bases Cata http://www.ncbi.nlm.nih.gov/ncicgap.

1 (National Cancer Institute / National Institute of Neurological National Cancer Institute / National Enstitute of Neurological National Stroke, Brain Tumor Genome Anatomy Project Disorders and Stroke, Brain Tumor Genome Anatomy Project Contact Robert Strausberg, Ph.D.

1 (Cata National 1998 this sequence version replaced gi:3035534.

1 (On Apr 7, 1998 this sequence version replaced gi:3035534.

1 (Only Apr 7, 1998 this sequence version replaced gi:3035534.

1 (Solid 496-1550)

2 Email: Robert Strausberg@nih.gov, M.D., Myrna R. Rosenfeld M.D., Prisue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seg_documentation_block: 729 bp mRNA EST 21-DEC-1999
LOCUS A1817709 TOL_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2413364 3'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone-"IMAGE:2413364"
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                                                                                                        .LeuargseraladlyCysSerLeuCysSeraladlyT 91
                                                                                                                                                                                                                                                                                                                                             108 SerSerThrProArgAlaLeuGluLeuArgGlyGlnSerGln 122
                                                                                                                                                                                                                                                                                                                                                                                           /organism-"Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence.
AI817709
AI817709.1 GI:5436788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_name: gb_est25:AI817709
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    ORGANISM
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AUTHORS
TITLE
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COMMENT
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VERSION
KEYWORDS
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caps: 2 percent Identity: 55.462

308.00 3.348 77.311

Quality:

Ratio: Percent Similarity: alignment_scores:

Length:

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AL Unpublished (1997) sequence version replaced gi:3036438.
On Apr 7, 1998 this sequence version replaced gi:3036438.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Tel: (301) 496-1550
Tel: (301) 496-1550
Tel: (301) 496-1550
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., M. Fatima
CDR Library Preparation: M. Bento Soares, Ph.D., M. Fatima
CDR Library Arrayed by: Greg Lennon, Ph.D.
CDR Sequencing Conternon
Content Library Arrayed by: Greg Lennon, Ph.D.
CDR Sequencing Conternon
Content Library Arrayed by: Greg Lennon, Ph.D.
CDR Sequencing Conternon
CDR Library Arrayed by: Greg Lennon, Ph.D.
CDR CONTENT Arrayed by: Greg Lenn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_documentation_block: 528 bp mRNA spiens cDNA clone IMAGE:2242420 3'
LOGUS A1638416
DEFINITION t131903.11 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:244420 3'
DEFINITION t131903.11 NCI_CGAP_GC6 HOMO SADIENS CLONE REGULATOR BETA FORM similar to TR:016361 016361 CELL CYCLE NEGARIVE REGULATOR BETA FORM ; contains to TR:016361 016361 cell contains in mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
1 (bases 1 to 528)
1 (Class http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Tumor Gene Index
Organization (Company Project (CGAP), Tumor Gene Index
Organization (Company Project (CGAP), Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11111 ::: 111 | 111::: 111 | 111::: 111 | 113 | 111 | 113 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    70 gGlyHisGlnAspileValArgTyrLeuArgSerAlaGlyCysSerLeuC 87
                                                                                                                                                                              20 ncysGluAspProThrThrPheSerArgProValHisAspAlaAlaArgG 37
                                                                                                                      20
                                                                                                                             4 GlyAsnValHisValAlaAlaLeuLeuLeuAsnTyrGlyAlaAspSerAs
to reverse of: A1817709 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A1638416
A1638416.1 GI:4690650
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us-09-016-869a-6.rst

source

FEATURES

BASE COUNT ORIGIN

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                                                                                                                                                                                                                                                                                                                                       CDNA Library Arrayed by: Greg Lennon, Ph.D.

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:

Seq primer: -400P from Glico . 0.00

High quality sequence stop: 454.

Localin/Qualifiers

Localin/Qualifiers
                                                                                                                      Tunor Gene Index Universell Genome Anatomy Project (GGAP), Optibilished (1997)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Tanall: Robert Strausberg@nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael CDA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
                                                  1 (bases 1 to 531)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     478 GGCCACTCTCACCCGACCGTGCACGCTGCTGCCGGGAGGGCTTCCTGG 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24 oThrThrPheSerArgProValHisAspAlaAlaArgGluGlyPheLeuA 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 ValalaalaLeuLeuAsnTyrGlyalaaspSerAsnCysGluAspPr 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58 AlaTrpClyArgLeuProLeuAspLeuAlaGlnGluArgGlyHisGlnAs 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91 rpSerLeuCysThrAlaGlyAsnValAlaGlnThrAspGlyH1sSerPhe 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            74 pilevalargTyrLeuArgSerAlaGlyCysSerLeuCysSerAlaClyT 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to reverse of: A1633790 from: 1 to: 531
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Percent Identity: 56.522
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US-09-016-869A-6 x AI633790/rev
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3.420
76.522
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Ratio:
Percent Similarity:
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                                                                    AUTHORS
TITLE
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COMMENT
                                       REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURES
                                                                                                                                                                                /notes"Vector: pt773D-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library NI_CGAP_GC4 was prepared, and ss circles were made in tracer in a subtractive hybridization this DNA was used as was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (clonelDs 1257096-1258631, Bento Soares and N. Fatima Bonaldo.), Subtraction by a 143 c 163 g 114 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A1633790 531 bp mRNA EST 14-DEC-1999

**LESBELO:X1 NCI_CGAP_GC6 Homo sapiens CDNA clone IMAGE:2242122 3/

**Similar to TR:Q16361 Q16361 CELL CYCLE NEGATIVE REGULATOR BETA FORM

**Contains LTR9.b3 TAR1 repetitive element ;/ mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8 ValAlaAlaLeuLeuLeuAsnTyrGlyAlaAspSerAsnCysGluAspPr 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41 spThrLeuValValLeuHisGlySerGlyAlaArgLeuAspValArgAsp 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58 AlarrpGlyArgLeuProLeuAspLeuAlaGlnGluArgGlyHisGlnAs 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74 pilevalargiyrieuArgSeralaGiyCysSerLeuCysSerAlaGiyr 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        91 rpserLeuCysThrAlaGlyAsnValAlaGlnThrAspGlyH1sSerPhe 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_"IMAGE:224420"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to reverse of: Al638416 from: 1 to: 528
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                                       /organism="Homo saplens"
                                                                         _xref-"taxon:9606
Location/Qualifiers
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US-09-016-869A-6 x AI638416/rev
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Ratio: 3.420
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DEFINITION

ACCESSION VERSION KEYWORDS

RGANISM

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Bonaldo, Ph.D.

Bonaldo, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

CDNA Library Arrayed by: Washington University Genome Sequencing Center

DNA Sequencing by: Washington University Genome Sequencing Center

DNA Sequencing by: Washington University at:

Clone distribution: NCI-CGAP clone distribution information can be

Clone distribution information of the consortium of the
                                                                                                                                                                                                                                                                                                                                                                                                                                             A1954684 1 G1:574694

A2954684 1 G1:5746994

EST 08-MAR-2000

BST 08-MAR-2
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Tel: (301) 496-1550

Tel: Robert Strausberg@nih.gov

Email: Robert_Strausberg@nih.gov

Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael

R. Emmert-Buck, M.D., Ph.D.

R. Enmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota, Metazoa; Chordata; Catarrhini; Hominidae; Homo.

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (basea to 563)

NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

National Cancer Institute,
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/lab_host="DH10B"
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:247323"
/clone=11b="NCI_CGAP_GGE"
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AUTHORS
TITLE
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SOURCE

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/note-"Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with /note-"Organ: pooled; Site_1: Not I; Site_2: Eco RI; a modified polylinker; Site_1: Not I; Site_2: Eco RI; a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized Equal amounts of plasmid DNA in three normalized Libraries (fetal lung NBHI19W, testis NHT, and B-cell libraries (fetal lung NBHI19W, testis NHT, and B-cell NI_CGAP_GCB1) were made in NI_CGAP_GCB1) were mixed, and ss circles were made in NI_CGAP_GCB1) were mixed, and ss circles were made in tracer in a subtractive hybridication reaction. The driver tracer in a subtractive hybridication reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made
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On Apr 7, 1998 this sequence version replaced g1:3034533.
On Apr 7, 1998 this sequence version replaced g1:3034533.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausbergenih.gov for further information.
This clone is available royalty free through LLNL; contact the
This Consortium (info@image.llnl.gov) for further information.
INAGE CONSORTIUM (info@image.llnl.gov) for further information.
INGER Length: 581 fwd. Er from Amersham
Seq primer: -40m3 fwd. Er from Amersham
High quality sequence stop: 398.
High quality sequence stop: 398.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Butherla; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 526)

NOI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NOI-CGAP http://www.ncbi.nlm.cih.gov/ncicgap.
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LOCUS
LOCUS
DEFINITION 0112b04.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone
DEFINITION 0112b04.s1 Soares_NFL_T_GBC_S1 Homo sapiens CBLL CYCLE NEGATIVE
REGULATOR BETA FORM ;, mRNA sequence.
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                                                                                                                                                          67 aGlnGluArgGlyHisGlnAspIleValArgTyrLeuArgSerAlaGlyC 84
545 ATGATGATGGGCAGCGCCGAGTGGCGGAGCTGCTGCTGCTCCACGCGC 496
                                                       17 aAspSerAsnCysGluAspProThrThrPheSerArgProValHisAspA
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/lab_host="DH10B"
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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Unpublished (1997)
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